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OM protein - protein search, using sw model

Run on: March 7, 2006, 17:40:32 ; Search time 11.7198 Seconds
(without alignments) 1087.222 Million cell updates/sec

Title: US-09-938-406-1_COPY_523_551

Perfect score: 139
Sequence: 1 AVGMGLGAMFLGLGAGTGTGATSWALTV 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*

1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	100.0	269	2	AAY22833 SEQ ID NO
2	139	100.0	269	5	ABG68304 Envelope
3	139	100.0	269	6	ABU57711 Human imm
4	139	100.0	649	2	Aaw44250 HIV-1 gp1
5	139	100.0	865	2	Aaw43072 HIV-1 gp1
6	131	94.2	669	6	ABP73114 Amino aci
7	131	94.2	669	6	ABP73117 Amino aci
8	131	94.2	669	6	ABP73122 Amino aci
9	131	94.2	669	6	ABP73120 Amino aci
10	131	94.2	844	6	ABP73115 Amino aci
11	131	94.2	844	6	ABP73112 Amino aci
12	131	94.2	844	6	ABP73118 Amino aci
13	131	94.2	844	6	ABP73121 Amino aci
14	131	94.2	844	6	ABP73111 Amino aci
15	130	93.5	791	9	ADK39690 HIV Env p
16	130	93.5	883	4	AB82761 Ancestral
17	130	93.5	883	9	ADW38347 Ancestral
18	130	93.5	883	9	ADY27998 HIV-1 gro
19	130	93.5	883	9	ABE10654 AN1-EnvB
20	130	93.5	883	9	ABE10552 HIV-1, su
21	129	92.8	267	2	AAY22831 SEQ ID NO
22	129	92.8	267	5	ABG68302 Envelope
23	129	92.8	267	6	ABU57709 Human imm
24	129	92.8	855	9	ADK39676 HIV Env p

25	128	92.1	269	2	AAY22851	Aay22851	SEQ ID NO
26	128	92.1	269	5	ABG68322	Envelope	
27	128	92.1	269	6	ABU57729	Human imm	
28	127	91.4	269	2	AAY22816	SEQ ID NO	
29	127	91.4	269	5	ABG68287	Envelope	
30	127	91.4	269	6	ABU57694	Human imm	
31	127	91.4	855	2	Aaw43069	HIV-1 gp1	
32	126	90.6	269	2	AAY22836	SEQ ID NO	
33	126	90.6	269	2	AAY22848	SEQ ID NO	
34	126	90.6	269	2	AAY22829	SEQ ID NO	
35	126	90.6	269	5	ABG68300	Envelope	
36	126	90.6	269	5	ABG68307	Envelope	
37	126	90.6	269	5	ABG68319	Envelope	
38	126	90.6	269	6	ABU57707	Human imm	
39	126	90.6	269	6	ABU57726	Human imm	
40	126	90.6	269	6	ABU57714	Human imm	
41	126	90.6	360	6	ABR57596	HIV gp41	
42	126	90.6	850	9	ADK39673	HIV Env p	
43	126	90.6	855	9	ADK39674	HIV Env p	
44	126	90.6	857	2	AAR12261	HIV-1 str	
45	125	89.9	269	2	AAY22825	SEQ ID NO	

ALIGNMENTS

RESULT 1

AAY22833
ID AAY22833 standard; protein; 269 AA.
XX
AC AAY22833;
XX
DT 19-AUG-1999 (first entry)
XX
DE SEQ ID NO. 29 from WO9820036.
XX
KW HIV; gp41 protein; constrained helical peptide; HIV infection; vaccine;
KW antibody; viral membrane fusion; viral infectivity;
KW ligand affinity purification; protein A replacement;
KW immunoglobulin purification; epitope mimic.
XX
OS Human immunodeficiency virus.
XX
FN WO9820036-A1.
XX
PD 14-MAY-1998.
XX
PF 05-NOV-1997; 97WO-US020069.
XX
PR 06-NOV-1996; 96US-00743698.
XX
PA 16-JUN-1997; 97US-00876698.
XX
(GETH) GENENTECH INC.
PI Braisted A, Judice JK, McDowell RS, Pheilan JC, Starovasmik MA;
PI Wells JA;
XX
DR WPI; 1998-286866/25.
XX
PT Production of constrained helical peptide(s) by linking side chains on
PT terminus of octapeptide - derived from human immunodeficiency virus gp41
PT protein, useful in vaccines for treatment and prevention of infection.
XX
PS Claim 11; Page 170; 279pp; English.
XX
CC Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus
CC (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins of
CC known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY22888 and
CC AAY22903 represent consensus sequences of various sections of the gp41
CC protein). Sequences derived from the peptides are used to produce
CC constrained helical peptides of the invention. The constrained helical
CC peptide is produced by synthesizing an octapeptide in which both terminal
CC amino acids have a side-chain that includes a group able to form an amide

CC bond, and cyclizing the octapeptide by reacting the specified side-chain
 CC residues with a difunctional linker to produce two amide bonds. The
 CC constrained helical peptides are used to treat or prevent HIV infection,
 CC especially as vaccines that generate antibodies that prevent viral
 CC membrane fusion or infectivity. Vaccines may contain constrained helical
 CC peptides derived from several different strains of HIV. The antibodies
 CC are also useful for diagnosing HIV infection. Other uses for the
 CC constrained helical peptides are in affinity purification of ligands
 CC (particularly where complete binding protein is not readily available,
 CC e.g. replacements for protein A in immunoglobulin purification); as
 CC epitope mimics for antibody production; for isolation of synthetic
 CC antibody clones from phage display libraries, or as stable forms of
 CC "floppy" peptides or proteins
 XX
 SQ Sequence 269 AA;

Query Match 100.0%; Score 139; DB 2; Length 269;
 Best Local Similarity 100.0%; Pred. No. 9.2e-11;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
 DB 42 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 70

RESULT 2
 ABG68304
 ID ABG68304 standard; protein; 269 AA.
 XX
 AC ABG68304;
 XX
 DT 29-AUG-2003 (revised)
 DT 07-OCT-2002 (first entry)
 XX
 DE Envelope protein gp41 from HIV clade B strain #23.
 XX
 KW HIV; glycoprotein; gp41; antigen; helical conformation;
 KW virus-induced membrane fusion; acquired immunodeficiency syndrome; AIDS;
 KW viral envelope protein; vaccine; virucide; anti-HIV.
 XX
 OS Human immunodeficiency virus 1; clade B.
 XX
 PN US6271198-B1.
 XX
 PD 07-AUG-2001.
 XX
 PF 05-NOV-1997; 97US-00965056.
 XX
 PR 06-NOV-1996; 96US-00743698.
 PR 16-JUN-1997; 97US-0049787P.
 PR 16-JUN-1997; 97US-00876698.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;
 PI Wells JA;
 XX
 DR WPI; 2002-487624/52.
 XX
 DR New cyclic peptides from human immune deficiency virus gp41, useful for
 PT treatment or prevention of HIV infection, are constrained to have alpha-
 PT helical conformation.
 XX
 PS Disclosure; Col 173-176; 175pp; English.
 XX
 CC The invention relates to cyclic peptides (A) with a constrained helical
 CC conformation, derived from gp41 (glycoprotein 41, a viral envelope
 CC protein) protein of human immunodeficiency virus (HIV). The cyclic
 CC peptides have formulas given in the specification part of which are
 CC derived from a consensus sequence of gp41 derived from HIV clades A, B,
 CC D, E or O. The peptides are used to cause induction of a specific
 CC immune response, resulting in antibodies that prevent virus-induced
 CC membrane fusion. The peptides are used to treat subjects with, or at risk

CC of, HIV infection, either as antifusion/anti-infection agents or,
 CC preferably where associated with a carrier, as an immunogen (including as
 CC vaccine) to raise antibodies. The antibodies may be used for diagnosis or
 CC prevention/treatment of HIV infection (i.e. acquired immunodeficiency
 CC syndrome, AIDS), e.g. prevention of mother-to-child transmission or in
 CC cases of health care accidents. The peptides can be based on specific HIV
 CC strains, e.g. breakthrough isolates of HIV that have developed during
 CC vaccine trials, so a combination of them should cover a wide range of
 CC protection. The present sequence is gp41 protein from a particular HIV
 CC clade used to derive a consensus sequence of gp41. (Updated on 29-AUG--
 CC 2003 to standardise OS field)
 XX
 SQ Sequence 269 AA;

Query Match 100.0%; Score 139; DB 5; Length 269;
 Best Local Similarity 100.0%; Pred. No. 9.2e-11;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
 DB 42 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 70

RESULT 3
 ABU57711
 ID ABU57711 standard; protein; 269 AA.
 XX
 AC ABU57711;
 XX
 DT 10-APR-2003 (first entry)
 DT
 XX Human immunodeficiency virus (HIV) envelope protein gp41 #23.
 DE
 XX Human immunodeficiency virus; HIV; vaccine; helical peptide compound;
 KW viral membrane fusion; hapten; immunogen; peptidomimetic; gp41;
 KW envelope protein.
 XX
 OS Human immunodeficiency virus.
 XX
 PN US2002151473-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 15-MAY-2001; 2001US-00854816.
 XX
 PR 06-NOV-1996; 96US-00743698.
 PR 16-JUN-1997; 97US-0049787P.
 PR 16-JUN-1997; 97US-00876698.
 PR 05-NOV-1997; 97US-00965056.
 XX
 PA (BRAI/) BRAISTED A C.
 PA (JUDI/) JUDICE J K.
 PA (MCDO/) MCDOWELL R S.
 PA (PHEL/) PHELAN J C.
 PA (STAR/) STAROVASNIK M A.
 PA (WELL/) WELLS J A.
 XX
 PI Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;
 PI Wells JA;
 XX
 DR WPI; 2003-182525/18.
 XX

PT Novel constrained helical peptide compound useful for prophylactically or
 PT therapeutically treating mammal at risk for or infected with human
 PT immunodeficiency virus.
 XX
 PS Disclosure; Fig 16; 180pp; English.

CC The invention describes a constrained helical peptide compound (I)
 CC comprising a first constrained helical peptide comprising a sequence of 8
 CC amino acids (a.as) having a first and second terminal residue both
 CC flanking an internal sequence of 6 a.as, where the terminal residues have
 CC a side chain that are linked to each other forming a locking group to

CC form a constrained helical peptide. (I) is useful for preparing
 CC antibodies that prevent viral membrane fusion, as happens, preferably
 CC attached to a carrier, for use as an immunogen to raise antibodies that
 CC have a diagnostic use, as a vaccine for treatment of patients at risk of
 CC or infected with HIV, to create combinatorial constrained helical peptide
 CC libraries that are useful in chemical selection systems, to isolate the
 CC binding determinants from alpha-helical binding domains of known
 CC proteins, for determining whether a binding determinate in an alpha-
 CC helical binding domain of a known protein can serve as a structural model
 CC for the design of peptidomimetics, to replace intact binding proteins or
 CC protein binding domains in the affinity purification of ligands, to mimic
 CC epitopes in proteins to selectively raise polyclonal or monoclonal
 CC antibodies against such individual epitopes for isolating synthetic
 CC antibody clones with a selected binding activity from phage display
 CC combinatorial libraries, to provide conformationally stable variants of
 CC peptides or proteins which exhibit floppy or unstable alpha-helical
 CC secondary structure at one or more sites in unrestrained form under
 CC conditions of interest. This is the amino acid sequence of an HIV
 CC envelope protein gp41, fragments of which are used in the creation of
 CC locked helix peptides

XX Sequence 269 AA;
 CC Query Match 100.0%; Score 139; DB 6; Length 269;
 CC Best Local Similarity 100.0%; Pred. No. 9.2e-11;
 CC Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
 Db 42 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 70

RESULT 4
 AAW44250
 ID AAW44250 standard; protein; 649 AA.

XX AC AAW44250;
 DT 17-OCT-2003 (revised)
 DT 26-JUN-1998 (first entry)
 XX HIV-1 gp160 residues 33-681.
 XX Vaccine; antibody; antigen; hydrophobic; proteosome; pathogen;
 XX immune response; sexually transmitted disease; HIV; infection.
 XX Human immunodeficiency virus 1.

XX Key Location/Qualifiers
 FH Region 491..519
 FT /note= "hydrophobic region"

XX WO9801558-A2.
 XX 15-JAN-1998.
 XX 10-JUL-1997; 97WO-US012253.
 XX 10-JUL-1996; 96US-0021687P.
 XX (INTE-) INTELLIVAX INC.
 XX (JACK-) JACKSON FOUND HENRY M.
 XX (USSA) US SEC OF ARMY.

XX Lowell GH, Vancott TC, Birs DL;
 XX WPI; 1998-110231/10.

XX Vaccine compositions for eliciting neutralising antibodies - comprising
 XX antigen containing hydrophobic sequence or having added hydrophobic
 XX material, complexed to proteosomes or bio-adhesive nano-emulsions.
 XX Claim 9; Page 22; 62pp; English.

XX The present sequence represents HIV-1 gp160 residues 33-681 (the full
 CC protein is on the SWISS-PROT database Seq ID: 119434) used in a vaccine
 CC of the present invention. The vaccine composition is capable of eliciting
 CC neutralising antibodies in a subject to a pathogenic organism which
 CC antibodies are present in vaginal secretions, intestinal secretions, lung
 CC secretions or faeces. The vaccine comprises: (a) an antigen comprising a
 CC protein or peptide having: (i) an endogenous hydrophobic sequence of 3-50
 CC non-polar or uncharged amino acids; (ii) added to the protein or peptide,
 CC an exogenous hydrophobic material comprising a sequence of 3 to 50 non-
 CC polar or uncharged amino acids or a 8-18C fatty acyl group, or (iii) both
 CC (i) and (ii), and (b) complexed with the antigen, a composition
 CC comprising proteosomes, bioadhesive nano-emulsions or both, where the
 CC complexed or coupled protein or peptide maintains a native structure of
 CC antigenic epitopes such that, upon administration to the subject, the
 CC antigen induces neutralising antibodies in one or more of vaginal
 CC secretions, intestinal secretions, lung secretions and faeces, capable of
 CC neutralising the pathogenic organism. The compositions can be used for
 CC inducing an immune response against a pathogenic organism such as a
 CC causative agent of a sexually-transmitted or mucosally-transmitted
 CC disease, e.g. HIV infection. The compositions preserve the antigenic
 CC integrity of the protein or peptide epitopes while at the same time
 CC enhancing their immunogenicity. (Updated on 17-OCT-2003 to standardise OS
 CC field)

XX Sequence 649 AA;
 CC Query Match 100.0%; Score 139; DB 2; Length 649;
 CC Best Local Similarity 100.0%; Pred. No. 2.3e-10;
 CC Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
 Db 491 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 519

RESULT 5
 AAW43072
 ID AAW43072 standard; peptide; 865 AA.

XX AC AAW43072;
 DT 17-OCT-2003 (revised)
 DT 11-SEP-1998 (first entry)
 XX HIV-1 gp120 protein fragment from isolate CDC4.

XX gp120 protein; purification; fractionation; ion exchange; chromatography;
 KW binding affinity; CD4; hydrophobic interaction; size exclusion; vaccine.

XX Human immunodeficiency virus 1.

XX US5696238-A.

XX 09-DEC-1997.

XX 11-MAY-1995; 95US-00439286.

XX 20-AUG-1991; 91US-00684963.

XX 16-AUG-1993; 93US-00109002.

XX 09-MAY-1994; 94US-00240073.

XX (CHIR) CHIRON CORP.

XX Scandella C, Haigwood NL;

XX WPI; 1998-041353/04.

XX Purification of HIV gp120 - using chromatographic methods.

XX Disclosure; Fig 2A-W; 53pp; English.

XX AAW43066-W43080 are fragments of the gp120 protein from different human

CC immunodeficiency virus type 1 (HIV-1) isolates. These proteins are used
 CC in a novel method for purifying HIV gp120 so as to provide a purified
 CC gp120 glycoprotein having protein/protein binding properties
 CC substantially identical to natural viral HIV gp120. The method involves
 CC fractionating a crude gp120 preparation containing full-length,
 CC glycosylated gp120 using ion exchange chromatography so as to provide a
 CC first collection of fractions. A fraction from the first collection is
 CC selected that exhibits specific binding affinity for CD4 peptide, thereby
 CC producing a first fractionated material. The first fractionated material
 CC is fractionated by hydrophobic interaction chromatography so as to
 CC provide a second collection of fractions from which a second collection
 CC is selected that exhibits specific binding affinity for CD4 peptide. This
 CC second fraction is fractionated by size exclusion chromatography so as to
 CC provide a third collection of fractions exhibiting specific binding
 CC affinity for CD4 peptide, thereby providing the purified gp120. The
 CC purified gp120 can be used for antibody production and in vaccines.
 CC (Updated on 17-OCT-2003 to standardise OS field)
 XX
 XX
 SQ Sequence 865 AA;

Query Match 100.0%; Score 139; DB 2; Length 865;
 Best Local Similarity 100.0%; Pred. No. 3.1e-10; Indels 0; Gaps 0;
 Matches 29; Conservative 0; Mismatches 0;

Qy 1 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 29
 |||||
 Db 521 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 549
 |||||

RESULT 6
 ABP73114
 ID ABP73114 standard; protein; 669 AA.

AC ABP73114;

XX 17-JUN-2003 (first entry)

XX Amino acid sequence of a HIV-1 envelope protein mutant gp140.

DE Envelope glycoprotein; HIV-1; isolate 133; vaccine; HIV infection; g12;
 KW gp140.

XX Synthetic.

OS Human immunodeficiency virus 1.

XX WO2003020755-A1.

XX 13-MAR-2003.

XX 06-SEP-2002; 2002WO-FR003039.

XX 06-SEP-2001; 2001FR-00011699.

XX (INMR) BIOMERIEUX SA.

XX Bedin F, Reynard F, Verrier B, Ataman-Oenal Y;

XX WPI; 2003-278759/27.

XX N-PSDB; ACC43017.

XX New mutated env gene of human immune deficiency virus, useful for genetic
 PT vaccination, also derived polypeptides having asparagine replaced by
 PT glutamine.

XX Claim 17; Page 91-94; 127pp; French.

XX The present sequence represents a truncated variant, designated gp140, of
 CC the Human immunodeficiency virus type 1 (HIV-1) isolate 133 envelope
 CC glycoprotein mutant g12 (see ACC43015 and ABP73112). The specification
 CC describes mutated HIV-1 envelope glycoproteins that have at least two
 CC mutations at glycosylation sites, conserved among primary isolates, each
 CC consisting of replacement of AAC or AAT (for Asn) by CAG or CAA (for
 CC Gln). The mutated envelope glycoprotein polynucleotides and polypeptides

CC are used in vaccines for prevention and treatment of HIV infection
 XX
 SQ Sequence 669 AA;

Query Match 94.2%; Score 131; DB 6; Length 669;
 Best Local Similarity 93.1%; Pred. No. 2.9e-09;
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 29
 |||||
 Db 499 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 527
 |||||

RESULT 7

ID ABP73117 standard; protein; 669 AA.

XX ABP73117;

XX 17-JUN-2003 (first entry)

XX Amino acid sequence of a HIV-1 envelope protein mutant gp140.

XX Envelope glycoprotein; HIV-1; isolate 133; vaccine; HIV infection; g112;
 KW gp140.

XX Synthetic.

OS Human immunodeficiency virus 1.

XX WO2003020755-A1.

XX 13-MAR-2003.

XX 06-SEP-2002; 2002WO-FR003039.

XX 06-SEP-2001; 2001FR-00011699.

XX (INMR) BIOMERIEUX SA.

XX Bedin F, Reynard F, Verrier B, Ataman-Oenal Y;

XX WPI; 2003-278759/27.

XX N-PSDB; ACC43020.

XX New mutated env gene of human immune deficiency virus, useful for genetic
 PT vaccination, also derived polypeptides having asparagine replaced by
 PT glutamine.

XX Claim 20; Page 99-102; 127pp; French.

XX The present sequence represents a truncated variant, designated gp140, of
 CC the Human immunodeficiency virus type 1 (HIV-1) isolate 133 envelope
 CC glycoprotein mutant g112 (see ACC43018 and ABP73115). The specification
 CC describes mutated HIV-1 envelope glycoproteins that have at least two
 CC mutations at glycosylation sites, conserved among primary isolates, each
 CC consisting of replacement of AAC or AAT (for Asn) by CAG or CAA (for
 CC Gln). The mutated envelope glycoprotein polynucleotides and polypeptides
 CC are used in vaccines for prevention and treatment of HIV infection

XX Sequence 669 AA;

Query Match 94.2%; Score 131; DB 6; Length 669;
 Best Local Similarity 93.1%; Pred. No. 2.9e-09;
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 29
 |||||
 Db 499 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 527
 |||||

RESULT 8

ID ABP73122 standard; protein; 669 AA.

```

XX AC ABP73122;
XX DT 17-JUN-2003 (first entry)
XX DE Amino acid sequence of a HIV-1 envelope protein mutant.
XX KW Envelope glycoprotein; HIV-1; vaccine; HIV infection.
XX OS Synthetic.
XX OS Human immunodeficiency virus 1.
XX PN WO2003020755-A1.
XX FD 13-MAR-2003.
XX PF 06-SEP-2002; 2002WO-FR003039.
XX PR 06-SEP-2001; 2001FR-00011699.
XX FA (INMR ) BIOMERIEUX SA.
XX PI Bedin F, Reynard F, Verrier B, Ataman-Oenal Y;
XX DR WPI; 2003-278759/27.
XX DR N-PSDB; ACC43025.
XX PT New mutated env gene of human immune deficiency virus, useful for genetic
XX PT vaccination, also derived polypeptides having asparagine replaced by
XX PS glutamine.
XX PS Claim 12; Page 108-110; 127pp; French.
XX CC The present sequence represents a truncated variant, designated gp140, of
XX CC the human immunodeficiency virus type 1 (HIV-1) isolate 133 envelope
XX CC glycoprotein mutant g14 (see ACC43021 and ABP731118). The specification
XX CC describes mutated HIV-1 envelope glycoproteins that have at least two
XX CC mutations at glycosylation sites, conserved among primary isolates, each
XX CC consisting of replacement of AAC or AAT (for Asn) by CAG or CAA (for
XX CC Gln). The mutated envelope glycoprotein polynucleotides and polypeptides
XX CC are used in vaccines for prevention and treatment of HIV infection
XX SQ Sequence 669 AA;

Query Match 94.2%; Score 131; DB 6; Length 669;
Best Local Similarity 93.1%; Pred. No. 2.9e-09;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAGSTMGATSMALTV 29
Db 499 AVGMGLGAMFLGFLGAGSTMGAAASLALTV 527
|||||
RESULT 10
ABP73115
ID ABP73115 standard; protein; 844 AA.
XX AC ABP73115;
XX DT 17-JUN-2003 (first entry)
XX DE Amino acid sequence of HIV-1 envelope protein mutant g112.
XX KW Envelope glycoprotein; HIV-1; isolate 133; vaccine; HIV infection; g112.
XX OS Synthetic.
XX OS Human immunodeficiency virus 1.
XX PN WO2003020755-A1.
XX PD 13-MAR-2003.
XX PF 06-SEP-2002; 2002WO-FR003039.
XX PR 06-SEP-2001; 2001FR-00011699.
XX FA (INMR ) BIOMERIEUX SA.
XX PI Bedin F, Reynard F, Verrier B, Ataman-Oenal Y;
XX DR WPI; 2003-278759/27.
XX DR N-PSDB; ACC43018.
XX OS New mutated env gene of human immune deficiency virus, useful for genetic
XX OS PT vaccination, also derived polypeptides having asparagine replaced by
XX OS PT glutamine.
XX PS Claim 20; Page 94-97; 127pp; French.
XX PS The present sequence represents the Human immunodeficiency virus type 1
XX CC

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CC (HIV-1) isolate 133 envelope glycoprotein mutant g112. The specification
 CC describes mutated HIV-1 envelope glycoproteins that have at least two
 CC mutations at glycosylation sites, conserved among primary isolates, each
 CC consisting of replacement of AAC or AAT (for Asn) by CAG or CAA (for
 CC Gln). The mutated envelope glycoprotein polynucleotides and polypeptides
 CC are used in vaccines for prevention and treatment of HIV infection
 XX
 SQ Sequence 844 AA;

Query Match 94.2%; Score 131; DB 6; Length 844;
 Best Local Similarity 93.1%; Pred. No. 3.7e-09;
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAGSTWGAATSMALTY 29
 |||||
 Db 499 AVGMGLGAMFLGFLGAGSTWGAATSMALTY 527

RESULT 11
 ABP73112
 ID ABP73112 standard; protein; 844 AA.

AC ABP73112;
 XX
 DT 17-JUN-2003 (first entry)

XX Amino acid sequence of HIV-1 envelope protein mutant g12.

XX Envelope glycoprotein; HIV-1; isolate 133; vaccine; HIV infection; g12.

OS Synthetic.
 OS Human immunodeficiency virus 1.

XX WO2003020755-A1.

XX 13-MAR-2003.

XX 06-SEP-2002; 2002WO-FR003039.

XX 06-SEP-2001; 2001FR-00011699.

XX (INMR) BIOMERIEUX SA.

XX Bedin F, Reynard F, Verrier B, Ataman-Oenal Y;

XX WPI; 2003-278759/27.

XX N-PSDB; ACC43015.

XX New mutated env gene of human immune deficiency virus, useful for genetic
 PT vaccination, also derived polypeptides having asparagine replaced by
 PT glutamine.

XX Claim 17; Page 85-89; 127pp; French.

XX The present sequence represents the Human immunodeficiency virus type 1
 CC (HIV-1) isolate 133 envelope glycoprotein mutant g12. The specification
 CC describes mutated HIV-1 envelope glycoproteins that have at least two
 CC mutations at glycosylation sites, conserved among primary isolates, each
 CC consisting of replacement of AAC or AAT (for Asn) by CAG or CAA (for
 CC Gln). The mutated envelope glycoprotein polynucleotides and polypeptides
 CC are used in vaccines for prevention and treatment of HIV infection
 XX

XX Sequence 844 AA;

Query Match 94.2%; Score 131; DB 6; Length 844;
 Best Local Similarity 93.1%; Pred. No. 3.7e-09;
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAGSTWGAATSMALTY 29
 |||||
 Db 499 AVGMGLGAMFLGFLGAGSTWGAATSMALTY 527

RESULT 12
 ABP73118

ID ABP73118 standard; protein; 844 AA.

XX ABP73118;

XX 17-JUN-2003 (first entry)

XX Amino acid sequence of HIV-1 envelope protein mutant g14.

XX Envelope glycoprotein; HIV-1; isolate 133; vaccine; HIV infection; g14.

OS Synthetic.

OS Human immunodeficiency virus 1.

XX WO2003020755-A1.

XX 13-MAR-2003.

XX 06-SEP-2002; 2002WO-FR003039.

XX 06-SEP-2001; 2001FR-00011699.

XX (INMR) BIOMERIEUX SA.

XX Bedin F, Reynard F, Verrier B, Ataman-Oenal Y;

XX WPI; 2003-278759/27.

XX N-PSDB; ACC43021.

XX New mutated env gene of human immune deficiency virus, useful for genetic
 PT vaccination, also derived polypeptides having asparagine replaced by
 PT glutamine.

XX Claim 12; Page 102-103; 127pp; French.

XX The present sequence represents the Human immunodeficiency virus type 1
 CC (HIV-1) isolate 133 envelope glycoprotein mutant g14. The specification
 CC describes mutated HIV-1 envelope glycoproteins that have at least two
 CC mutations at glycosylation sites, conserved among primary isolates, each
 CC consisting of replacement of AAC or AAT (for Asn) by CAG or CAA (for
 CC Gln). The mutated envelope glycoprotein polynucleotides and polypeptides
 CC are used in vaccines for prevention and treatment of HIV infection
 XX

XX Sequence 844 AA;

Query Match 94.2%; Score 131; DB 6; Length 844;
 Best Local Similarity 93.1%; Pred. No. 3.7e-09;
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAGSTWGAATSMALTY 29
 |||||
 Db 499 AVGMGLGAMFLGFLGAGSTWGAATSMALTY 527

RESULT 13
 ABP73121

ID ABP73121 standard; protein; 844 AA.

XX ABP73121;

XX 17-JUN-2003 (first entry)

XX Amino acid sequence of a HIV-1 envelope protein mutant.

XX Envelope glycoprotein; HIV-1; vaccine; HIV infection.

OS Synthetic.

OS Human immunodeficiency virus 1.

XX WO2003020755-A1.

XX 13-MAR-2003.

XX 06-SEP-2002; 2002WO-FR003039.
XX
XX
PR 06-SEP-2001; 2001FR-00011699.
XX
XX (INNR) BIOMERIEUX SA.
XX
XX
PI Bedin F, Reynard F, Verrier B, Ataman-Oenal Y;
XX
XX WPI; 2003-278759/27.
DR N-PSDB; ACC43024.
XX
XX New mutated env gene of human immune deficiency virus, useful for genetic
PT vaccination, also derived polypeptides having asparagine replaced by
PT glutamine.
XX
XX Disclosure; Page 113-116; 127pp; French.
XX
XX The present sequence represents a Human immunodeficiency virus type 1
CC (HIV-1) envelope glycoprotein mutant. The specification describes mutated
CC HIV-1 envelope glycoproteins that have at least two mutations at
CC glycosylation sites, conserved among primary isolates, each consisting of
CC replacement of AAC or AAT (for Asn) by CAG or CAA (for Gln). The mutated
CC envelope glycoprotein polynucleotides and polypeptides are used in
CC vaccines for prevention and treatment of HIV infection
XX
XX Sequence 844 AA;
SQ

Query Match 94.2%; Score 131; DB 6; Length 844;
Best Local Similarity 93.1%; Pred. No. 3.7e-09;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy 1 AVGMGLAMFLGFLGAGSTMGATSMALTV 29
Db 499 AVGMGLAMFLGFLGAGSTMGATSMALTV 527

RESULT 14
ABP73111
ID ABP73111 standard; protein; 844 AA.
XX
XX AC ABP73111;
XX
XX DT 23-OCT-2003 (revised)
XX DT 17-JUN-2003 (first entry)
XX
XX Amino acid sequence of the envelope protein of HIV-1 isolate 133.
XX
XX Envelope glycoprotein; HIV-1; isolate 133; vaccine; HIV infection; gene.
XX
XX Human immunodeficiency virus 1.
XX
XX WO2003020755-A1.
XX
XX FD 13-MAR-2003.
XX
XX 06-SEP-2002; 2002WO-FR003039.
XX
XX 06-SEP-2001; 2001FR-00011699.
XX
XX (INNR) BIOMERIEUX SA.
XX
XX Bedin F, Reynard F, Verrier B, Ataman-Oenal Y;
XX
XX WPI; 2003-278759/27.
DR N-PSDB; ACC43014.
XX
XX New mutated env gene of human immune deficiency virus, useful for genetic
PT vaccination, also derived polypeptides having asparagine replaced by
PT glutamine.
XX
XX Disclosure; Page 82-85; 127pp; French.
XX

CC The present sequence represents an envelope glycoprotein of Human
CC immunodeficiency virus type 1 (HIV-1) isolate 133. The specification
CC describes mutated HIV-1 envelope glycoproteins that have at least two
CC mutations at glycosylation sites, conserved among primary isolates, each
CC consisting of replacement of AAC or AAT (for Asn) by CAG or CAA (for
CC Gln). The mutated envelope glycoprotein polynucleotides and polypeptides
CC are used in vaccines for prevention and treatment of HIV infection.
CC (Updated on 23-OCT-2003 to standardise OS field)
XX
XX Sequence 844 AA;
SQ

Query Match 94.2%; Score 131; DB 6; Length 844;
Best Local Similarity 93.1%; Pred. No. 3.7e-09;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy 1 AVGMGLAMFLGFLGAGSTMGATSMALTV 29
Db 499 AVGMGLAMFLGFLGAGSTMGATSMALTV 527

RESULT 15
ADX39690
ID ADX39690 standard; protein; 791 AA.
XX
XX AC ADX39690;
XX
XX DT 21-APR-2005 (first entry)
XX
XX HIV Env protein #99.
XX
XX Immune stimulation; Env.
XX
XX Human immunodeficiency virus.
XX
XX WO2005012502-A2.
XX
XX PD 10-FEB-2005.
XX
XX 29-MAR-2004; 2004WO-US009510.
XX
XX 28-MAR-2003; 2003US-0458026P.
XX
XX (EPIM-) EPIMUNE INC.
XX
XX Baker DM, Livingston BD, Chesnut RW, Sette A, Newman MJ;
XX
XX WPI; 2005-132661/14.
XX
XX Identifying a candidate peptide epitope, which induces a HLA class I CTL
PT response comprises identifying variants of a peptide epitope 8-11 amino
PT acids in length comprising primary anchor residues of the same HLA class
PT I binding motif.
XX
XX Disclosure; Page 180-231; 458pp; English.
XX
XX The invention relates to a method of identifying a candidate peptide
CC epitope which induces an HLA class I CTL response against variants of the
CC peptide epitope, comprising identifying, from a particular antigen of an
CC infectious agent, variants of a peptide epitope comprising primary anchor
CC residues of the same HLA class I binding motif. The method is useful for
CC identifying a candidate peptide epitope, which induces an HLA class I CTL
CC response against variants of the peptide epitope. This sequence
CC represents an HIV Env protein used in the scope of the invention.
XX
XX Sequence 791 AA;
SQ

Query Match 93.5%; Score 130; DB 9; Length 791;
Best Local Similarity 93.1%; Pred. No. 4.7e-09;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1 AVGMGLAMFLGFLGAGSTMGATSMALTV 29
Db 514 AVGMGLAMFLGFLGAGSTMGATSMALTV 542

Search completed: March 7, 2006, 17:45:24
Job time : 12.7198 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	139	100.0	868	1	VCLJH4	env polyprotein -
2	127	91.4	861	1	VCLJSC	env polyprotein pr
3	124	89.2	69	2	S60706	env protein - huma
4	123	88.5	69	2	S60690	env protein - huma
5	122	87.8	358	2	S70417	envelope protein g
6	122	87.8	358	2	S22000	envelope protein g
7	122	87.8	358	2	S22002	envelope protein g
8	120	86.3	855	1	VCLJ42	env polyprotein pr
9	119	85.6	856	1	VCLJ3W	env polyprotein pr
10	116	83.5	69	2	S60689	env protein - huma
11	114	82.0	69	2	S60691	env protein - huma
12	113.5	81.7	294	2	S60525	envelope polyprot
13	111.5	80.2	68	2	S60693	env protein - huma
14	110.5	79.5	854	2	S13288	env protein - huma
15	110.5	79.5	859	2	T01672	envelope polyprot
16	109.5	78.8	357	2	S22004	-envelope protein g
17	109.5	78.8	357	2	S22006	envelope protein g
18	109.5	78.8	851	2	S33985	env polyprotein -
19	109.5	78.8	853	2	S54384	envelope polyprot
20	109.5	78.8	855	1	VCLJZR	env polyprotein pr
21	109.5	78.8	856	1	VCLJH3	env polyprotein pr
22	109.5	78.8	856	1	VCLJVL	env polyprotein pr
23	108.5	78.1	68	2	S60696	env protein - huma
24	108.5	78.1	301	2	S60532	envelope polyprot
25	108.5	78.1	301	2	S60531	envelope polyprot
26	108.5	78.1	357	2	S21994	envelope protein g
27	108.5	78.1	445	2	A41621	env polyprotein M
28	108.5	78.1	847	2	T09448	envelope glycopro
29	108.5	78.1	847	2	S13289	env protein - huma

A;Gene: env

Df 511 AVGAIGAMFLGFLGAAGSTMGAASLTTLTV 539

RESULT 10
S60689
env protein - human immunodeficiency virus type 1 (isolate 2051) (fragment)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: S60689
R:Rojas, J.M.; Dopazo, J.; Najera, I.; Sanchez-Palomino, S.; Olivares, I.; Martin, M.J.;
Virus Res. 31, 331-342, 1994
A>Title: Molecular epidemiology of HIV-1 in Madrid.
A:Reference number: S60687; MUID:94249284; PMID:7545926
A:Accession: S60689
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-69 <ROJ>
A:Cross-references: UNIPROT:Q76152; UNIPARC:UPI000010A870; EMBL:Z29691; NID:g808979; PID:
C:Superfamily: type E retrovirus env polyprotein

Query Match 83.5%; Score 116; DB 2; Length 69;
Best Local Similarity 79.3%; Pred. No. 1.7e-08;
Matches 23; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 1 AVGMIGAMFLGFLGAAGSTMGAATSLTTLTV 29
|||||:|||||||:|||||:|||||
Db 8 AVGMIGAVFLGFLGAAGSTMGARSLTTLTV 36

RESULT 11
S60691
env protein - human immunodeficiency virus type 1 (isolate D5/-2) (fragment)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: S60691
R:Rojas, J.M.; Dopazo, J.; Najera, I.; Sanchez-Palomino, S.; Olivares, I.; Martin, M.J.;
Virus Res. 31, 331-342, 1994
A>Title: Molecular epidemiology of HIV-1 in Madrid.
A:Reference number: S60687; MUID:94249284; PMID:7545926
A:Accession: S60691
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-69 <ROJ>
A:Cross-references: UNIPROT:Q76154; UNIPARC:UPI0000107C1C; EMBL:Z29919; NID:g808983; PID:
C:Superfamily: type E retrovirus env polyprotein

Query Match 82.0%; Score 114; DB 2; Length 69;
Best Local Similarity 75.9%; Pred. No. 3e-08;
Matches 22; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 1 AVGMIGAMFLGFLGAAGSTMGAATSLTTLTV 29
|||||:|||||||:|||||:|||||
Db 8 AVGVIGALFGLGAGSTMGARALTTLTV 36

RESULT 12
S60525
envelope glycoprotein gp41 - human immunodeficiency virus type 1 (isolate CI-13-3 and iso
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate CI-13-3; isolate CI-13-4
C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S60525; S60527
R:Janseens, W.; Heyndrickx, L.; Van de Peer, Y.; Bouckaert, A.; Franssen, K.; Motte, J.;
AIDS 8, 21-26, 1994
A>Title: Molecular phylogeny of part of the env gene of HIV-1 strains isolated in Cote d
A:Reference number: S60521; MUID:94280700; PMID:8011235
A:Accession: S60525
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-294 <JAN>
A:Cross-references: UNIPROT:Q76169; UNIPROT:Q76170; UNIPARC:UPI0000102742; EMBL:X72028; I
A:Experimental source: isolate CI-13-3
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, May 1993

A;Accession: S60527
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-294 <JAW>
A;Cross-references: UNIPARC:UPI0000102742; EMBL:X7029; NID:g468633; PIDN:CAA50912.1; PT
A;Experimental source: isolate CI-13-4
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; glycoprotein; immunodeficiency; polyprotein

Query Match 81.7%; Score 113.5; DB 2; Length 294;
Best Local Similarity 86.2%; Pred. No. 1.4e-07;
Matches 25; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 AVGNLGNMFLGFLGAAGSTWGCATSMALT V 29
| : | | | | | | | | | | | | | | | | | | | |
Db 237 AIG-LGAMFLGFLGAAGSTWGAASMTLT V 264

RESULT 13
S60693
env protein - human immunodeficiency virus type 1 (isolate 306) (fragment)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S60693
R;Rojas, J.M.; Dopazo, J.; Najera, I.; Sanchez-Palomino, S.; Olivares, I.; Martin, M.J.;
Virus Res. 31, 331-342, 1994
A;Title: Molecular epidemiology of HIV-1 in Madrid.
A;Reference number: S60687; MUID:94249284; PMID:7545926
A;Accession: S60693
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-68 <ROJ>
A;Cross-references: UNIPROT:Q76157; UNIPARC:UPI000010B1F0; EMBL:Z29684; NID:g808989; PID
C;Superfamily: type E retrovirus env polyprotein

```
Query Match      80.2%; Score 111.5; DB 2; Length 68;  
Best Local Similarity 86.2%; Pred. NO. 6.3e-08;  
Matches 25; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
```

QY 1 AVGMLGAMFLGFLGAAGSTMGATSMALTIV 29
 |||||
Db 8 AVG-IGMFLGLQAAGSTMGARSWTLTV 35

RESULT 14
S13288
env protein - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type_1, HIV-1
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Dec-2004
C/Accession: S13288
R/O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.
Nature 348, 69-73, 1990
A/TITLE: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A/Reference number: S13288; PMID:2172833
A/Accession: S13288
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-854 <OBR>
A/Cross-references: UNIPROT: Q85582; UNIPROT: Q72502; UNIPROT: O90178; UNIPROT: C078243; UNIRP:

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Query Match          79.5%; Score 110.5; DB 2; Length 854;
Best Local Similarity 82.8%; Pred. No. 1e-06;
Matches 24; Conservative 2; Mismatches 2; Indels 1; Gaps 1;
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RESULT 15

T01672
envelope polyprotein precursor - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01672
R:Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
Cell 46, 63-74, 1986
A:Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isolates
A:Reference number: Z14389; MUID:86245056; PMID:2424612
A:Accession: T01672
A:Status: preliminary; translated from GB/EMBL/DBDB
A:Molecule type: mRNA
A:Residues: 1-859 <ALI>
A:Cross-references: UNIPROT:P04583; UNIPARC:UPI000002C1CF; EMBL:K03456; NID:g60228; PIDN
C:Superfamily: type E retrovirus env polyprotein

Query Match 79.5%; Score 110.5; DB 2; Length 859;
Best Local Similarity 82.8%; Pred. No. 1e-06;
Matches 24; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 AVGMIGAMFLGFLGAAGSTWGCATSMALT 29
| : | | | | | | | | | | | | | | | | | | | |
Db 514 AIG-LGAMFLGFLGAAGSTWGAASLTIV 541

Search completed: March 7, 2006, 17:51:35
Job time : 3.22419 secs

GenCore version 5.1.7
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OM protein - protein search, using sw_model

Run on: March 7, 2006, 17:40:55 ; Search time 13.3024 Seconds
(without alignments)
1538.097 Million cell updates/sec

Title: US-09-938-406-1_COPY_523_551
Perfect score: 139
Sequence: 1 AVGMGLMFLGFLGAGSTGATSMALTV 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	100.0	868	1 ENV HVIC4	P05879 human immun
2	132	95.0	877	2 Q6IUG0	Q6IUG0 human immun
3	132	95.0	877	2 Q6IUG1	Q6IUG1 human immun
4	132	95.0	877	2 Q6IUG2	Q6IUG2 human immun
5	131	94.2	799	2 Q6QLJ1	Q6QLJ1 human immun
6	131	94.2	814	2 Q6QLK5	Q6QLK5 human immun
7	131	94.2	844	2 Q6QLK7	Q6QLK7 human immun
8	131	94.2	844	2 Q6QLK8	Q6QLK8 human immun
9	131	94.2	844	2 Q6QLK9	Q6QLK9 human immun
10	131	94.2	844	2 Q6QLJ0	Q6QLJ0 human immun
11	131	94.2	844	2 Q6QLJ4	Q6QLJ4 human immun
12	131	94.2	859	2 Q6QLJ5	Q6QLJ5 human immun
13	131	94.2	859	2 Q6QLJ6	Q6QLJ6 human immun
14	131	94.2	859	2 Q6QLJ7	Q6QLJ7 human immun
15	131	94.2	859	2 Q6QLJ8	Q6QLJ8 human immun
16	131	94.2	859	2 Q6QLJ9	Q6QLJ9 human immun
17	131	94.2	859	2 Q6QLK0	Q6QLK0 human immun
18	131	94.2	859	2 Q6QLK1	Q6QLK1 human immun
19	131	94.2	859	2 Q6QLK2	Q6QLK2 human immun
20	131	94.2	859	2 Q6QLK3	Q6QLK3 human immun
21	131	94.2	859	2 Q6QLK4	Q6QLK4 human immun
22	131	94.2	859	2 Q6QLK6	Q6QLK6 human immun
23	131	94.2	859	2 Q6QLK7	Q6QLK7 human immun
24	131	94.2	868	2 Q6QLK3	Q6QLK3 human immun
25	130	93.5	858	2 Q7SUT2	Q7SUT2 human immun
26	130	93.5	858	2 P87924	P87924 human immun
27	130	93.5	859	2 Q7SUT4	Q7SUT4 human immun
28	130	93.5	859	2 Q7SUT6	Q7SUT6 human immun
29	130	93.5	859	2 Q7SUT7	Q7SUT7 human immun
30	130	93.5	859	2 Q7SUT8	Q7SUT8 human immun
31	130	93.5	859	2 Q7SUT9	Q7SUT9 human immun

32	130	93.5	865	2 Q7SUT5	Q7SUT5 human immun
33	129	92.8	855	1 ENV HVIC4	ENV HVIC4
34	128	92.1	797	2 Q03808	Q03808 human immun
35	128	92.1	797	2 Q03810	Q03810 human immun
36	128	92.1	799	2 Q03807	Q03807 human immun
37	128	92.1	801	2 Q03809	Q03809 human immun
38	128	92.1	852	2 Q69992	Q69992 human immun
39	128	92.1	857	2 Q7ZJ87	Q7ZJ87 human immun
40	128	92.1	857	2 Q9DQ26	Q9DQ26 human immun
41	128	92.1	858	2 Q9PY30	Q9PY30 human immun
42	128	92.1	861	2 Q7SUV9	Q7SUV9 human immun
43	127	91.4	387	2 Q6JE18	Q6JE18 human immun
44	127	91.4	844	2 Q6QLL2	Q6QLL2 human immun
45	127	91.4	848	2 Q6HIR8	Q6HIR8 human immun

ALIGNMENTS

RESULT 1

ID ENV HVIC4 STANDARD; PRT; 868 AA.
AC P05879;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
DE Name=ENV;
GN Human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1).
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11687;
RN [1]
RP NUCLEOTIDE SEQUENCE
RX MEDLINE=87041461; PubMed=34906666;
RA Desai S.M., Kalyanaram V.S., Casey J.M., Srinivasan A.,
RA Andersen P.R., Devare S.G.;
RT "Molecular cloning and primary nucleotide sequence analysis of a
RT distinct human immunodeficiency virus isolate reveal significant
RT divergence in its genomic sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384 (1986).
[2]
RN PROTEIN SEQUENCE OF 34-43.
RP MEDLINE=90253924; PubMed=2187500;
RA Kalyanaram V.S., Rodriguez V., Veronese F., Rahman R., Lusso P.,
RA DeVico A.L., Copeland T., Oroszian S., Gallo R.C., Sarngadharan M.G.;
RT "Characterization of the secreted, native gp120 and gp160 of the human
RT immunodeficiency virus type 1";
RL AIDS Res. Hum. Retroviruses 6:371-380 (1990).

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

EMBL: M13137; AAA44311.1; -; Genomic_RNA.

PIR: C25523; VCLJH4.

HSP: P19549; IMEQ.

SMR: P05879; 84-128, 87-212, 206-503, 552-638.

HIV: M13137; ENV5CDC45.

InterPro: IPR000328; Env GP41.

InterPro: IPR000777; GP120.

Pfam: PF00516; GP120; 1.

Pfam: PF00517; GP41; 1.

AIDS; Capsid protein; Direct protein sequencing; Glycoprotein;

Polyprotein; Signal; Structural protein; Transmembrane.

CHAIN 1 33 Exterior membrane glycoprotein.

CHAIN 34 522 Transmembrane glycoprotein.

CARBOHYD 523 868 N-linked (GlcNAc...) (potential).

CARBOHYD 89 89 N-linked (GlcNAc...) (potential).

CARBOHYD 131 131

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FT CARBOHYD 138 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 139 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 142 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 162 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 166 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 195 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 198 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 208 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 245 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 252 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 273 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 287 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 300 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 306 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 312 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 342 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 349 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 365 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 371 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 395 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 405 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 409 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 459 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 473 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 623 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 628 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 637 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 649 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 828 N-linked (GlcNAc. . .) (Potential).
FT DISULFID 55 By similarity.
FT DISULFID 120 By similarity.
FT DISULFID 127 By similarity.
FT DISULFID 132 By similarity.
FT DISULFID 229 By similarity.
FT DISULFID 239 By similarity.
FT DISULFID 307 By similarity.
FT DISULFID 387 By similarity.
FT DISULFID 394 By similarity.
SQ SEQUENCE 868 AA; 98699 MW; A11527FC52A6F0C8 CRC64;

Query Match 100.0%; Score 139; DB 1; Length 868;
Best Local Similarity 100.0%; Pred. No. 28-09;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
Db 523 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 551

RESULT 2
Q6IUG0_9HIV1
ID Q6IUG0_9HIV1 PRELIMINARY; PRT; 877 AA.
AC Q6IUG0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Envelope glycoprotein.
GN Name-env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gorby P.R., Kunstman K.J., Morgan T., Moore J.P., Mascola J.R.,
RA Agopian K., Holm G.H., Mehle A., Taylor J., Farzan M., Wang H.,
RA Ellery P., Willey S., Clapham P., Wolinsky S.M., Crowe S.M.,
RA Gabuzda D.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV624307; AAT4420.1; -; Genomic_DNA.
DR HSSP; P04578; IK33.
DR SMR; P04578; 80-134, 561-647.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env.GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Envelope protein; Transmembrane.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 877 AA; 99339 MW; 81FF9C9641E832C CRC64;

Query Match 95.0%; Score 132; DB 2; Length 877;
Best Local Similarity 93.1%; Pred. No. 1.6e-08;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
Db 532 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 560

RESULT 4
Q6IUG2_9HIV1
ID Q6IUG2_9HIV1 PRELIMINARY; PRT; 877 AA.
AC Q6IUG2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Envelope glycoprotein.
GN Name-env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
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DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env.GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 877 AA; 99229 MW; D5F0E3B9A831EE3F CRC64;

Query Match 95.0%; Score 132; DB 2; Length 877;
Best Local Similarity 93.1%; Pred. No. 1.6e-08;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
Db 532 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 560

RESULT 3
Q6IUG1_9HIV1
ID Q6IUG1_9HIV1 PRELIMINARY; PRT; 877 AA.
AC Q6IUG1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Envelope glycoprotein.
GN Name-env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gorby P.R., Kunstman K.J., Morgan T., Moore J.P., Mascola J.R.,
RA Agopian K., Holm G.H., Mehle A., Taylor J., Farzan M., Wang H.,
RA Ellery P., Willey S., Clapham P., Wolinsky S.M., Crowe S.M.,
RA Gabuzda D.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV624306; AAT4419.1; -; Genomic_DNA.
DR HSSP; P04578; IK33.
DR SMR; P04578; 80-134, 561-647.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env.GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Envelope protein; Transmembrane.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 877 AA; 99339 MW; 81FF9C9641E832C CRC64;

Query Match 95.0%; Score 132; DB 2; Length 877;
Best Local Similarity 93.1%; Pred. No. 1.6e-08;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 29
Db 532 AVGMGLGAMFLGFLGAAGSTMGATSMALTV 560

RESULT 4
Q6IUG2_9HIV1
ID Q6IUG2_9HIV1 PRELIMINARY; PRT; 877 AA.
AC Q6IUG2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Envelope glycoprotein.
GN Name-env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
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Db 499 AVGMLGAMFLGLGAAGSTMGAASLALTV 527

RESULT 6
Q6QLK5_9H1V1
ID Q6QLK5_9H1V1 PRELIMINARY; PRT; 814 AA.
AC Q6QDK5;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC Primate lentivirus group.
ON NCBI_TaxID=11676;
RX [1]_TaxID=11676;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=133;
RX PubMed=15507649; DOI=10.1128/JVI.78.22.12625-12637.2004;
RA Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.,
RT "Evolutionary Dynamics of the Glycan Shield of the Human
RT Immunodeficiency Virus Envelope during Natural Infection and
RT Implications for Exposure of the 2G12 Epitope."; J. Virol. 78:12625-12637(2004).
RL EMBL; AY535434; AAS58777.1; -; Genomic_RNA.
DR SMR; Q6QLK5; 200-494, 543-629.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR Pfam; PF00424; REV; 1.
KW Envelope protein.
SQ SEQUENCE: 814 AA; 91785 MW; 8AAB45FF6CA6953A1 CRC64;

Query Match 94.2%; Score 131; DB 2; Length 814;
Best Local Similarity 93.1%; Pred. No. 2e-08;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps

QY 1 AVGMLGAMFLGLGAAGSTMGATSWALTV 29
|||||
DB 514 AVGMLGAMFLGLGAAGSTMGAASLALTV 542
|||||

RESULT 7
Q56561_9H1V1
ID Q56561_9H1V1 PRELIMINARY; PRT; 844 AA.
AC Q56561;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentiviruses; Primate lentivirus group.
ON NCBI_TaxID=11676;
RX [1]_TaxID=11676;
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=59372987; PubMed=10445815; DOI=10.1089/088922299310548;
RA Ataman-Onal Y., Coiffier C., Giraud A., Babic-Erceg A., Biron F.,
RA Verrier B.;
RT "Comparison of complete env gene sequences from individuals with
RT symptomatic primary HIV type 1 infection."; AIDS Res. Hum. Retroviruses 15:1035-1039(1999).
RL AIDS Res. Hum. Retroviruses 15:1035-1039(1999).
DR EMBL; AF0411126; AAC02517.1; -; Genomic_DNA.
DR HSSP; P04578; 1K34.


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Db 499 AVGMGLAMFLGFLGAAGSTMGAASLALTV 527

RESULT 11
ID Q6QLJ4_9HIV1 PRELIMINARY; PRT; 844 AA.
AC Q6QLJ4_9HIV1 PRELIMINARY; PRT; 844 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=133;
RX PubMed=15507649; DOI=10.1128/JVI.78.22.12625-12637.2004;
RA Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.;
RT "Evolutionary Dynamics of the Glycan Shield of the Human
RT Immunodeficiency Virus Envelope during Natural Infection and
RT Implications for Exposure of the 2G12 Epitope.";
RL J. Virol. 78.12625-12637(2004).
DR EMBL; AY354429; AAS58772.1; -; Genomic_RNA.
DR SMR; Q6QLJ4; 140-479, 528-614.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 844 AA; 95807 MW; 17A31D1BD9CF0ADC CRC64;

Query Match 94.2%; Score 131; DB 2; Length 844;
Best Local Similarity 93.1%; Pred. No. 2.1e-08;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLAMFLGFLGAAGSTMGAASLALTV 29
Db 499 AVGMGLAMFLGFLGAAGSTMGAASLALTV 527

RESULT 12
ID Q6QLJ4_9HIV1 PRELIMINARY; PRT; 859 AA.
AC Q6QLJ4_9HIV1 PRELIMINARY; PRT; 859 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=133;
RX PubMed=15507649; DOI=10.1128/JVI.78.22.12625-12637.2004;
RA Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.;
RT "Evolutionary Dynamics of the Glycan Shield of the Human
RT Immunodeficiency Virus Envelope during Natural Infection and
RT Implications for Exposure of the 2G12 Epitope.";
RL J. Virol. 78.12625-12637(2004).
DR EMBL; AY354446; AAS58789.1; -; Genomic_RNA.
DR SMR; Q6QLJ4; 200-494, 543-629.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 859 AA; 97398 MW; 8378D387EA019CD2 CRC64;

Query Match 94.2%; Score 131; DB 2; Length 859;
Best Local Similarity 93.1%; Pred. No. 2.1e-08;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLAMFLGFLGAAGSTMGAASLALTV 29
Db 514 AVGMGLAMFLGFLGAAGSTMGAASLALTV 542

RESULT 13
ID Q6QLJ5_9HIV1 PRELIMINARY; PRT; 859 AA.
AC Q6QLJ5_9HIV1 PRELIMINARY; PRT; 859 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=133;
RX PubMed=15507649; DOI=10.1128/JVI.78.22.12625-12637.2004;
RA Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.;
RT "Evolutionary Dynamics of the Glycan Shield of the Human
RT Immunodeficiency Virus Envelope during Natural Infection and
RT Implications for Exposure of the 2G12 Epitope.";
RL J. Virol. 78.12625-12637(2004).
DR EMBL; AY353445; AAS58788.1; -; Genomic_RNA.
DR SMR; Q6QLJ5; 200-494, 543-629.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 859 AA; 97398 MW; 8378D387EA019CD2 CRC64;

Query Match 94.2%; Score 131; DB 2; Length 859;
Best Local Similarity 93.1%; Pred. No. 2.1e-08;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLAMFLGFLGAAGSTMGAASLALTV 29
Db 514 AVGMGLAMFLGFLGAAGSTMGAASLALTV 542

RESULT 14
ID Q6QLJ6_9HIV1 PRELIMINARY; PRT; 859 AA.
AC Q6QLJ6_9HIV1 PRELIMINARY; PRT; 859 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
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Job time : 14.3024 secs

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=133;
RX PubMed=15507649; DOI=10.1128/JVI.78.22.12625-12637.2004;
RA Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.;
RT "Evolutionary Dynamics of the Glycan Shield of the Human
RT Immunodeficiency Virus Envelope during Natural Infection and
RT Implications for Exposure of the 2G12 Epitope.";
RL J. Virol. 78:12625-12637(2004).
DR EMBL; AY535444; AAS58787.1; -; Genomic_RNA.
DR SMR; Q6QLJ6; 543-629.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 859 AA; 97581 MW; CDFE3D498277012B CRC64;

Query Match 94.2%; Score 131; DB 2; Length 859;
Best Local Similarity 93.1%; Pred. No. 2.1e-08;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVGMGLGMFLGFLGAGSTMGATSMALTV 29
DB 514 AVGMGLGMFLGFLGAGSTMGASLALTV 542

RESULT 15
Q6QLJ7_9HIV1
ID Q6QLJ7_9HIV1 PRELIMINARY; PRT; 859 AA.
AC Q6QLJ7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=133;
RX PubMed=15507649; DOI=10.1128/JVI.78.22.12625-12637.2004;
RA Dacheux L., Moreau A., Ataman-Onal Y., Biron F., Verrier B., Barin F.;
RT "Evolutionary Dynamics of the Glycan Shield of the Human
RT Immunodeficiency Virus Envelope during Natural Infection and
RT Implications for Exposure of the 2G12 Epitope.";
RL J. Virol. 78:12625-12637(2004).
DR EMBL; AY535442; AAS58785.1; -; Genomic_RNA.
DR SMR; Q6QLJ7; 200-494, 543-629.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 859 AA; 97483 MW; 5B54B76D5F4245A8 CRC64;

Query Match 94.2%; Score 131; DB 2; Length 859;
Best Local Similarity 93.1%; Pred. No. 2.1e-08;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVGMGLGMFLGFLGAGSTMGATSMALTV 29
DB 514 AVGMGLGMFLGFLGAGSTMGASLALTV 542

Search completed: March 7, 2006, 17:50:38
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 7, 2006, 17:51:03 ; Search time 3.03687 Seconds
(without alignments)
789.495 Million cell updates/sec

Title: US-09-938-406-1_COPY_523_551

Perfect score: 139

Sequence: 1 AVGMGLAMFLGLGAGSTWGATSMALTV 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	139	100.0	269	2	US-08-965-056-29
2	129	92.8	269	2	US-08-965-056-27
3	128	92.1	269	2	US-08-965-056-47
4	127	91.4	269	2	US-08-965-056-12
5	127	91.4	855	2	US-07-956-483-14
6	127	91.4	887	2	US-08-472-240A-5
7	126	90.6	269	2	US-08-965-056-25
8	126	90.6	269	2	US-08-965-056-32
9	126	90.6	269	2	US-08-965-056-44
10	125	89.9	269	2	US-08-965-056-21
11	124	89.2	79	2	US-08-965-056-58
12	124	89.2	269	2	US-08-965-056-36
13	124	89.2	269	2	US-08-965-056-43
14	124	89.2	269	2	US-08-965-056-46
15	123	88.5	269	2	US-08-965-056-31
16	123	88.5	269	2	US-08-965-056-42
17	122	87.8	269	2	US-08-965-056-6
18	122	87.8	269	2	US-08-965-056-23
19	122	87.8	269	2	US-08-965-056-24
20	121	87.1	105	2	US-08-965-056-52
21	121	87.1	105	2	US-08-965-056-54
22	120	86.3	40	2	US-08-948-782-3
23	120	86.3	40	2	US-09-482-612-3
24	120	86.3	40	2	US-09-677-554-3
25	120	86.3	269	2	US-08-965-056-28
26	120	86.3	269	2	US-08-965-056-30
27	120	86.3	269	2	US-08-965-056-45

28 120 86.3 610 2 US-09-257-490-12 Sequence 12, Appl
29 120 86.3 855 2 US-07-956-483-15 Sequence 15, Appl
30 120 86.3 887 2 US-08-472-240A-6 Sequence 6, Appl
31 118 84.9 79 2 US-08-965-056-60 Sequence 60, Appl
32 118 84.9 269 2 US-08-965-056-22 Sequence 22, Appl
33 118 84.9 880 1 US-08-788-815-7 Sequence 7, Appl
34 118 84.9 880 2 US-09-157-963-7 Sequence 7, Appl
35 118 84.9 880 2 US-09-568-105-7 Sequence 7, Appl
36 118 84.9 906 2 US-08-472-240A-3 Sequence 3, Appl
37 117 84.2 79 2 US-08-965-056-59 Sequence 59, Appl
38 117 84.2 269 2 US-08-965-056-34 Sequence 34, Appl
39 116 83.5 269 2 US-08-965-056-33 Sequence 33, Appl
40 116 83.5 270 2 US-08-965-056-67 Sequence 67, Appl
41 116 83.5 865 2 US-07-956-483-13 Sequence 13, Appl
42 116 83.5 887 2 US-08-472-240A-4 Sequence 4, Appl
43 114 82.0 269 2 US-08-965-056-37 Sequence 37, Appl
44 114 82.0 269 2 US-08-965-056-48 Sequence 48, Appl
45 114 82.0 269 2 US-08-965-056-76 Sequence 76, Appl

ALIGNMENTS

RESULT 1
US-08-965-056-29 ; Sequence 29, Application US/08965056
; Patent No. 6271198
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; APPLICANT: J. Kevin Judice
; APPLICANT: Robert S. McDowell
; APPLICANT: J. Christopher Phelan
; APPLICANT: Melissa A. Starovasnik
; APPLICANT: James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; TITLE OF INVENTION: Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,056
; FILING DATE: 05-No. 6271198-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Phd., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

US-08-965-056-29
Query Match 100.0%; Score 139; DB 2; Length 269;
Best Local Similarity 100.0%; Pred. No. 2.8e-12;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AVGMGLAMFLGLGAGSTWGATSMALTV 29
|||||

Db 42 AVGMGLAMFLGLGAAGSTMGATSMALTV 70

RESULT 2

US-08-965-056-27
; Sequence 27, Application US/08965056
; Patent No. 6271198

GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted
APPLICANT: J. Kevin Judice
APPLICANT: Robert S. McDowell
APPLICANT: J. Christopher Phelan
APPLICANT: Melissa A. Starovasnik
APPLICANT: James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of

TITLE OF INVENTION: Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/965,056

FILING DATE: 05-No. 6271198-1997

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, PhD., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 267 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-965-056-27

Query Match 92.8%; Score 129; DB 2; Length 267;

Best Local Similarity 93.1%; Pred. No. 7.5e-11;

Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVGMGLAMFLGLGAAGSTMGATSMALTV 29

Db 42 AVGMGLAMFLGLGAAGSTMGATSMALTV 70

RESULT 3

US-08-965-056-47

; Sequence 47, Application US/08965056

; Patent No. 6271198

GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

APPLICANT: J. Kevin Judice

APPLICANT: Robert S. McDowell

APPLICANT: J. Christopher Phelan

APPLICANT: Melissa A. Starovasnik

APPLICANT: James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of

TITLE OF INVENTION: Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/965,056

FILING DATE: 05-No. 6271198-1997

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, PhD., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 269 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-965-056-47

Query Match 92.1%; Score 128; DB 2; Length 269;

Best Local Similarity 89.7%; Pred. No. 1.1e-10;

Matches 26; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLAMFLGLGAAGSTMGATSMALTV 29

Db 42 AVGMGLAMFLGLGAAGSTMGATSMALTV 70

RESULT 4

US-08-965-056-12

; Sequence 12, Application US/08965056

; Patent No. 6271198

GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

APPLICANT: J. Kevin Judice

APPLICANT: Robert S. McDowell

APPLICANT: J. Christopher Phelan

APPLICANT: Melissa A. Starovasnik

APPLICANT: James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of

TITLE OF INVENTION: Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/965,056

FILING DATE: 05-No. 6271198-1997

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, PhD., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881


```
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,056
; FILING DATE: 05-No. 6271198-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Ph.D., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-965-056-25

Query Match          90.6%; Score 126; DB 2; Length 269;
Best Local Similarity 89.7%; Pred. No. 2.1e-10;
Matches 26; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTIV 29
Db 42 AVGLGAVFLGFLGAAGSTMGATSMALTIV 70

RESULT 8
US-08-965-056-32
; Sequence 32, Application US/08965056
; Patent No. 6271198
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; APPLICANT: J. Kevin Judice
; APPLICANT: Robert S. McDowell
; APPLICANT: J. Christopher Phelan
; APPLICANT: Melissa A. Starovashnik
; APPLICANT: James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; TITLE OF INVENTION: Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,056
; FILING DATE: 05-No. 6271198-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Ph.D., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-965-056-44

Query Match          90.6%; Score 126; DB 2; Length 269;
Best Local Similarity 89.7%; Pred. No. 2.1e-10;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTIV 29
Db 42 AVGLGAVFLGFLGAAGSTMGATSMALTIV 70

RESULT 9
US-08-965-056-44
; Sequence 44, Application US/08965056
; Patent No. 6271198
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; APPLICANT: J. Kevin Judice
; APPLICANT: Robert S. McDowell
; APPLICANT: J. Christopher Phelan
; APPLICANT: Melissa A. Starovashnik
; APPLICANT: James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; TITLE OF INVENTION: Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,056
; FILING DATE: 05-No. 6271198-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Ph.D., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-965-056-44

Query Match          90.6%; Score 126; DB 2; Length 269;
Best Local Similarity 89.7%; Pred. No. 2.1e-10;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTIV 29
Db 42 AVGLGAVFLGFLGAAGSTMGATSMALTIV 70

RESULT 10
US-08-965-056-21
; Sequence 21, Application US/08965056
; Patent No. 6271198
; GENERAL INFORMATION:
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```

; APPLICANT: Andrew C. Braisted
; APPLICANT: J. Kevin Judice
; APPLICANT: Robert S. McDowell
; APPLICANT: J. Christopher Phelan
; APPLICANT: Melissa A. Starovasnlik
; APPLICANT: James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; TITLE OF INVENTION: Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,056
; FILING DATE: 05-No. 6271198-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Phd., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-965-056-21

Query Match      89.9%; Score 125; DB 2; Length 269;
Best Local Similarity 89.7%; Pred. No. 2.9e-10;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAGSTMGATSMALTV 29
Db 42 AVGALGALFLGFLGAGSTMGASMALTV 70

RESULT 11
US-08-965-056-58
; Sequence 58, Application US/08965056
; Patent No. 6271198
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; APPLICANT: J. Kevin Judice
; APPLICANT: Robert S. McDowell
; APPLICANT: J. Christopher Phelan
; APPLICANT: Melissa A. Starovasnlik
; APPLICANT: James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; TITLE OF INVENTION: Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,056
; FILING DATE: 05-No. 6271198-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Phd., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 113
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-965-056-36

Query Match      89.9%; Score 125; DB 2; Length 269;
Best Local Similarity 89.7%; Pred. No. 2.9e-10;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAGSTMGATSMALTV 29
Db 42 AVGALGALFLGFLGAGSTMGASMALTV 70

RESULT 11
US-08-965-056-58
; Sequence 58, Application US/08965056
; Patent No. 6271198
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; APPLICANT: J. Kevin Judice
; APPLICANT: Robert S. McDowell
; APPLICANT: J. Christopher Phelan
; APPLICANT: Melissa A. Starovasnlik
; APPLICANT: James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; TITLE OF INVENTION: Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,056
; FILING DATE: 05-No. 6271198-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Phd., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-965-056-36

Query Match      89.2%; Score 124; DB 2; Length 269;
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; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA: US/08/965,056
; FILING DATE: 05-No. 6271198-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Phd., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-965-056-58

Query Match      89.2%; Score 124; DB 2; Length 79;
Best Local Similarity 89.7%; Pred. No. 9.8e-11;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAGSTMGATSMALTV 29
Db 42 AVGLGAMFLGFLGAGSTMGASVALTV 70

RESULT 12
US-08-965-056-36
; Sequence 36, Application US/08965056
; Patent No. 6271198
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; APPLICANT: J. Kevin Judice
; APPLICANT: Robert S. McDowell
; APPLICANT: J. Christopher Phelan
; APPLICANT: Melissa A. Starovasnlik
; APPLICANT: James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; TITLE OF INVENTION: Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,056
; FILING DATE: 05-No. 6271198-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Phd., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-965-056-36

Query Match      89.2%; Score 124; DB 2; Length 269;
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Best Local Similarity 89.7%; Pred. No. 4e-10;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 29
Db 42 AVGTGLGAMFLGFLGAAGSTMGAASMTLTV 70

RESULT 13
US-08-965-056-43
; Sequence 43, Application US/08965056
; Patent No. 6271198
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; APPLICANT: J. Kevin Judice
; APPLICANT: Robert S. McDowell
; APPLICANT: J. Christopher Phelan
; APPLICANT: Melissa A. Starovasnik
; APPLICANT: James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; TITLE OF INVENTION: Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,056
; FILING DATE: 05-No. 6271198-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Phd., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-965-056-46

Query Match 89.2%; Score 124; DB 2; Length 269;
Best Local Similarity 89.7%; Pred. No. 4e-10;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 29
Db 42 AVGTGLGAMFLGFLGAAGSTMGAASMTLTV 70

RESULT 14
US-08-965-056-46
; Sequence 46, Application US/08965056
; Patent No. 6271198
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; APPLICANT: J. Kevin Judice
; APPLICANT: Robert S. McDowell
; APPLICANT: J. Christopher Phelan
; APPLICANT: Melissa A. Starovasnik
; APPLICANT: James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of

; TITLE OF INVENTION: Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,056
; FILING DATE: 05-No. 6271198-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Phd., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-965-056-46

Query Match 89.2%; Score 124; DB 2; Length 269;
Best Local Similarity 89.7%; Pred. No. 4e-10;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 29
Db 42 AVGTGLGAMFLGFLGAAGSTMGAASMTLTV 70

RESULT 15
US-08-965-056-31
; Sequence 31, Application US/08965056
; Patent No. 6271198
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; APPLICANT: J. Kevin Judice
; APPLICANT: Robert S. McDowell
; APPLICANT: J. Christopher Phelan
; APPLICANT: Melissa A. Starovasnik
; APPLICANT: James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; TITLE OF INVENTION: Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,056
; FILING DATE: 05-No. 6271198-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Phd., Timothy E.

REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-965-056-31

Query Match 88.5%; Score 123; DB 2; Length 269;
Best Local Similarity 86.2%; Pred. No. 5.5e-10;
Matches 25; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVGNLGMFLGFLGAGSTMGATSMALTV 29
|||:|||||||
Db 42 AVGIIGAMFLGFLGAGSTMGARSMTLTV 70
|||:|||||||

Search completed: March 7, 2006, 17:52:52
Job time : 4.03687 secs

This Page Blank (uspto)

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 7, 2006, 17:51:52 ; Search time 9.4528 Seconds
(without alignments)
1281.847 Million cell updates/sec

Title: US-09-938-406-1_COPY_523_551

Perfect score: 139

Sequence: 1 AVGNLGMFLGFLGAGSTWGTSMALTV 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	100.0	269	3	US-09-854-816-29
2	139	100.0	868	3	US-09-938-406-1
3	131	94.2	669	5	US-10-487-094-14
4	131	94.2	669	5	US-10-487-094-17
5	131	94.2	669	5	US-10-487-094-20
6	131	94.2	669	5	US-10-487-094-25
7	131	94.2	844	5	US-10-487-094-11
8	131	94.2	844	5	US-10-487-094-12
9	131	94.2	844	5	US-10-487-094-15
10	131	94.2	844	5	US-10-487-094-18
11	131	94.2	844	5	US-10-487-094-24
12	130	93.5	883	4	US-10-441-926-2
13	130	93.5	883	4	US-10-441-949-2
14	130	93.5	883	5	US-10-780-507-2
15	130	93.5	883	5	US-10-780-507-121
16	129	92.8	267	3	US-09-854-816-27
17	128	92.1	269	3	US-09-854-816-47
18	127	91.4	269	3	US-09-854-816-12
19	126	90.6	269	3	US-09-854-816-25
20	126	90.6	269	3	US-09-854-816-32
21	126	90.6	269	3	US-09-854-816-44
22	126	90.6	360	4	US-10-214-670-60
23	125	89.9	269	3	US-09-854-816-21
24	124	89.2	79	3	US-09-854-816-58
25	124	89.2	269	3	US-09-854-816-36
26	124	89.2	269	3	US-09-854-816-43
27	124	89.2	269	3	US-09-854-816-46

28	124	89.2	862	5	US-10-780-507-50	Sequence 50, Appl
29	123	88.5	269	3	US-09-854-816-31	Sequence 31, Appl
30	123	88.5	269	3	US-09-854-816-42	Sequence 42, Appl
31	122	87.8	269	3	US-09-854-816-6	Sequence 6, Appl
32	122	87.8	269	3	US-09-854-816-23	Sequence 23, Appl
33	122	87.8	269	3	US-09-854-816-24	Sequence 24, Appl
34	121	87.1	105	3	US-09-854-816-32	Sequence 52, Appl
35	121	87.1	105	3	US-09-854-816-54	Sequence 54, Appl
36	121	87.1	848	5	US-10-844-858-1	Sequence 1, Appl
37	120	86.3	269	3	US-09-854-816-28	Sequence 28, Appl
38	120	86.3	269	3	US-09-854-816-30	Sequence 30, Appl
39	120	86.3	269	3	US-09-854-816-45	Sequence 45, Appl
40	120	86.3	862	5	US-10-780-507-51	Sequence 51, Appl
41	118	84.9	79	3	US-09-854-816-60	Sequence 60, Appl
42	118	84.9	269	3	US-09-854-816-22	Sequence 22, Appl
43	118	84.9	852	4	US-10-093-953A-29	Sequence 29, Appl
44	117	84.2	79	3	US-09-854-816-59	Sequence 59, Appl
45	117	84.2	269	3	US-09-854-816-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1

US-09-854-816-29
; Sequence 29, Application US/09854816
; Patent NO. US20020151473A1
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; J. Kevin Judice
; Robert S. McDowell
; J. Christopher Phelan
; Melissa A. Starovasinik
; James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/854,816
; FILING DATE: 15-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/965,056
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Phd., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-854-816-29
Query Match 100.0%; Score 139; DB 3; Length 269;
Best Local Similarity 100.0%; Pred. No. 2.5e-10;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAAGSTWGATSMALTV 29
|||||
Db 42 AVGMGLGAMFLGFLGAAGSTWGATSMALTV 70
|||||

RESULT 2

US-09-938-406-1
; Sequence 1, Application US/09938406
; Patent No. US20020155120A1
; GENERAL INFORMATION:
; APPLICANT: Lowell, George
; APPLICANT: Vancott, Thomas
; APPLICANT: Birk, Deborah
; TITLE OF INVENTION: PROTEIN AND PEPTIDE VACCINES FOR
; INDUCING MUCOSAL IMMUNITY
; FILE REFERENCE: 40646-20002.10
; CURRENT APPLICATION NUMBER: US/09/938,406
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/214,701
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/US 97/12253
; PRIOR FILING DATE: 1997-07-10
; PRIOR APPLICATION NUMBER: US 60/021,687
; PRIOR FILING DATE: 1996-07-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 868
; TYPE: PRT
; ORGANISM: Virus HIV-1
US-09-938-406-1

Query Match 100.0%; Score 139; DB 3; Length 868;
Best Local Similarity 100.0%; Pred. No. 8.6e-10;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAAGSTWGATSMALTV 29
|||||
Db 523 AVGMGLGAMFLGFLGAAGSTWGATSMALTV 551
|||||

RESULT 3

US-10-487-094-14
; Sequence 14, Application US/10487094
; Publication No. US20050065320A1
; GENERAL INFORMATION:
; APPLICANT: BEDIN, Frederic
; APPLICANT: REYNARD, Frederic
; APPLICANT: VERRIER, Bernard
; APPLICANT: ATAMAN-ONAL, Yasemin
; TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THEREOF
; FILE REFERENCE: 118745
; CURRENT APPLICATION NUMBER: US/10/487,094
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: FR 01/11699
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 669
; TYPE: PRT
; ORGANISM: HIV-1 mutant g12
US-10-487-094-14

Query Match 94.2%; Score 131; DB 5; Length 669;
Best Local Similarity 93.1%; Pred. No. 7.4e-09;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAAGSTWGATSMALTV 29
|||||
Db 499 AVGMGLGAMFLGFLGAAGSTWGATSMALTV 527
|||||

RESULT 4

US-10-487-094-17
; Sequence 17, Application US/10487094
; Publication No. US20050065320A1
; GENERAL INFORMATION:
; APPLICANT: BEDIN, Frederic
; APPLICANT: REYNARD, Frederic
; APPLICANT: VERRIER, Bernard
; APPLICANT: ATAMAN-ONAL, Yasemin
; TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THEREOF
; FILE REFERENCE: 118745
; CURRENT APPLICATION NUMBER: US/10/487,094
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: FR 01/11699
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 669
; TYPE: PRT
; ORGANISM: HIV-1 mutant g112
US-10-487-094-17

Query Match 94.2%; Score 131; DB 5; Length 669;
Best Local Similarity 93.1%; Pred. No. 7.4e-09;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAAGSTWGATSMALTV 29
|||||
Db 499 AVGMGLGAMFLGFLGAAGSTWGATSMALTV 527
|||||

RESULT 5

US-10-487-094-20
; Sequence 20, Application US/10487094
; Publication No. US20050065320A1
; GENERAL INFORMATION:
; APPLICANT: BEDIN, Frederic
; APPLICANT: REYNARD, Frederic
; APPLICANT: VERRIER, Bernard
; APPLICANT: ATAMAN-ONAL, Yasemin
; TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THEREOF
; FILE REFERENCE: 118745
; CURRENT APPLICATION NUMBER: US/10/487,094
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: FR 01/11699
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 669
; TYPE: PRT
; ORGANISM: HIV-1 mutant g14
US-10-487-094-20

Query Match 94.2%; Score 131; DB 5; Length 669;
Best Local Similarity 93.1%; Pred. No. 7.4e-09;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAAGSTWGATSMALTV 29
|||||
Db 499 AVGMGLGAMFLGFLGAAGSTWGATSMALTV 527
|||||

RESULT 6

US-10-487-094-25
; Sequence 25, Application US/10487094
; Publication No. US20050065320A1
; GENERAL INFORMATION:
; APPLICANT: BEDIN, Frederic
; APPLICANT: REYNARD, Frederic

```
; APPLICANT: VERRIER, Bernard
; APPLICANT: ATAMAN-ONAL, Yasemin
; TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THEREOF
; FILE REFERENCE: 118745
; CURRENT APPLICATION NUMBER: US/10/487,094
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: FR 01/11699
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 669
; TYPE: PRT
; ORGANISM: HIV-1 mutant g22
US-10-487-094-25

Query Match          94.2%; Score 131; DB 5; Length 669;
Best Local Similarity 93.1%; Pred. No. 7.4e-09;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 29
Db 499 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 527

RESULT 7
US-10-487-094-11
; Sequence 11, Application US/10487094
; Publication No. US20050065320A1
; GENERAL INFORMATION:
; APPLICANT: BEDIN, Frederic
; APPLICANT: REYNARD, Frederic
; APPLICANT: VERRIER, Bernard
; APPLICANT: ATAMAN-ONAL, Yasemin
; TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THEREOF
; FILE REFERENCE: 118745
; CURRENT APPLICATION NUMBER: US/10/487,094
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: FR 01/11699
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 844
; TYPE: PRT
; ORGANISM: HIV-1 133
US-10-487-094-11

Query Match          94.2%; Score 131; DB 5; Length 844;
Best Local Similarity 93.1%; Pred. No. 9.5e-09;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 29
Db 499 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 527

RESULT 8
US-10-487-094-12
; Sequence 12, Application US/10487094
; Publication No. US20050065320A1
; GENERAL INFORMATION:
; APPLICANT: BEDIN, Frederic
; APPLICANT: REYNARD, Frederic
; APPLICANT: VERRIER, Bernard
; APPLICANT: ATAMAN-ONAL, Yasemin
; TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THEREOF
; FILE REFERENCE: 118745
; CURRENT APPLICATION NUMBER: US/10/487,094
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: FR 01/11699
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 26
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 844
; TYPE: PRT
; ORGANISM: HIV-1 mutant g12
US-10-487-094-12

Query Match          94.2%; Score 131; DB 5; Length 844;
Best Local Similarity 93.1%; Pred. No. 9.5e-09;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 29
Db 499 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 527

RESULT 9
US-10-487-094-15
; Sequence 15, Application US/10487094
; Publication No. US20050065320A1
; GENERAL INFORMATION:
; APPLICANT: BEDIN, Frederic
; APPLICANT: REYNARD, Frederic
; APPLICANT: VERRIER, Bernard
; APPLICANT: ATAMAN-ONAL, Yasemin
; TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THEREOF
; FILE REFERENCE: 118745
; CURRENT APPLICATION NUMBER: US/10/487,094
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: FR 01/11699
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 844
; TYPE: PRT
; ORGANISM: HIV-1 mutant g112
US-10-487-094-15

Query Match          94.2%; Score 131; DB 5; Length 844;
Best Local Similarity 93.1%; Pred. No. 9.5e-09;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 29
Db 499 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 527

RESULT 10
US-10-487-094-18
; Sequence 18, Application US/10487094
; Publication No. US20050065320A1
; GENERAL INFORMATION:
; APPLICANT: BEDIN, Frederic
; APPLICANT: REYNARD, Frederic
; APPLICANT: VERRIER, Bernard
; APPLICANT: ATAMAN-ONAL, Yasemin
; TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THEREOF
; FILE REFERENCE: 118745
; CURRENT APPLICATION NUMBER: US/10/487,094
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: FR 01/11699
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 844
; TYPE: PRT
; ORGANISM: HIV-1 mutant g14
US-10-487-094-18

Query Match          94.2%; Score 131; DB 5; Length 844;
Best Local Similarity 93.1%; Pred. No. 9.5e-09;
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Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLAMFLGLGAAGSTMGTSMALTV 29
Db 499 AVGMGLAMFLGLGAAGSTMGTSMALTV 527

RESULT 11
US-10-487-094-24
; Sequence 24, Application US/10487094
; Publication No. US20050063320A1
; GENERAL INFORMATION:
; APPLICANT: BEDIN, Frederic
; APPLICANT: REYNARD, Frederic
; APPLICANT: VERRIER, Bernard
; APPLICANT: ATAMAN-ONAL, Yasemin
; TITLE OF INVENTION: MUTATED HIV-1 ENV GENE, MUTATED ENV GLYCOPROTEIN AND THE USE THEREOF
; FILE REFERENCE: 118745
; CURRENT APPLICATION NUMBER: US/10/487,094
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: FR 01/11699
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 844
; TYPE: PRT
; ORGANISM: HIV-1 mutant g22
US-10-487-094-24

Query Match 94.2%; Score 131; DB 5; Length 844;
Best Local Similarity 93.1%; Pred. No. 9.5e-09;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVGMGLAMFLGLGAAGSTMGTSMALTV 29
Db 499 AVGMGLAMFLGLGAAGSTMGTSMALTV 527

RESULT 12
US-10-441-926-2
; Sequence 2, Application US/10441926
; Publication No. US20040115621A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo, Allen
; APPLICANT: Ross, Howard A.
; APPLICANT: Mullins, James I.
; TITLE OF INVENTION: ANCESTRAL VIRUSES AND VACCINES
; FILE REFERENCE: 08987-011001
; CURRENT APPLICATION NUMBER: US/10/441,926
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: PCT/US01/05288
; PRIOR FILING DATE: 2001-02-18
; PRIOR APPLICATION NUMBER: US 60/183,659
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 883
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially generated peptide
US-10-441-926-2

Query Match 93.5%; Score 130; DB 4; Length 883;
Best Local Similarity 93.1%; Pred. No. 1.4e-08;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVGMGLAMFLGLGAAGSTMGTSMALTV 29
Db 538 AVGMGLAMFLGLGAAGSTMGTSMALTV 566

RESULT 13
US-10-441-949-2
; Sequence 2, Application US/10441949
; Publication No. US20040116684A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo, Allen
; APPLICANT: Ross, Howard A.
; APPLICANT: Mullins, James I.
; TITLE OF INVENTION: ANCESTRAL VIRUSES AND VACCINES
; FILE REFERENCE: 08987-012001
; CURRENT APPLICATION NUMBER: US/10/441,949
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: PCT/US01/05288
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 60/183,659
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 883
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially generated peptide
US-10-441-949-2

Query Match 93.5%; Score 130; DB 4; Length 883;
Best Local Similarity 93.1%; Pred. No. 1.4e-08;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVGMGLAMFLGLGAAGSTMGTSMALTV 29
Db 538 AVGMGLAMFLGLGAAGSTMGTSMALTV 566

RESULT 14
US-10-780-507-2
; Sequence 2, Application US/10780507
; Publication No. US20050137387A1
; GENERAL INFORMATION:
; APPLICANT: MULLINS, James I.
; APPLICANT: RODRIGO, Allen G.
; APPLICANT: LEARN, Gerald H.
; APPLICANT: LI, Fusheng
; APPLICANT: NICKLE, David C.
; APPLICANT: JENSEN, Mark A.
; TITLE OF INVENTION: ANCESTRAL AND GUT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 16336-001320US
; CURRENT APPLICATION NUMBER: US/10/780,507
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US 10/204,204
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: PCT/US01/05288
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 60/183,659
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/447,586
; PRIOR FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 883
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ancestral HIV-1 group M, subtype B, env sequence
US-10-780-507-2

Query Match 93.5%; Score 130; DB 5; Length 883;
Best Local Similarity 93.1%; Pred. No. 1.4e-08;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 AVGMGLGAMFLGLGAAGSTMGTGATSMALTV 29
Db 538 AVGMGLGAMFLGLGAAGSTMGTGASMTLTV 566

RESULT 15

US-10-780-507-121
; Sequence 121, Application US/10780507
; Publication No. US20050137387A1
; GENERAL INFORMATION:
; APPLICANT: MULLINS, James I.
; APPLICANT: RODRIGO, Allen G.
; APPLICANT: LEARN, Gerald H.
; APPLICANT: LI, Fusheng
; APPLICANT: NICKLE, David C.
; APPLICANT: JENSEN, Mark A.
; TITLE OF INVENTION: ANCESTRAL AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPO
; FILE REFERENCE: 16336-001320US
; CURRENT APPLICATION NUMBER: US/10/780,507
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US 10/204,204
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: PCT/US01/05288
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 60/183,659
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/447,586
; PRIOR FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 121
; LENGTH: 883
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Deduced ancestor env protein sequence
US-10-780-507-121

Query Match 93.5%; Score 130; DB 5; Length 883;
Best Local Similarity 93.1%; Pred. No. 1.4e-08;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVGMGLGAMFLGLGAAGSTMGTGATSMALTV 29
Db 538 AVGMGLGAMFLGLGAAGSTMGTGASMTLTV 566

Search completed: March 7, 2006, 17:56:39
Job time : 10.4528 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2006, 17:53:05 ; Search time 1.11209 Seconds
(without alignments)
521.549 Million cell updates/sec

Title: US-09-938-406-1_COPY_523_551

Perfect score: 139

Sequence: 1 AVGMGLAMFLGFLCAAGSTWGATSMALTV 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 135346 seqs, 20000420 residues

Total number of hits satisfying chosen parameters: 135346

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109.5	78.8	856	US-10-510-947-8	Sequence 8, Appl
2	109.5	78.8	856	US-11-042-988-13	Sequence 13, Appl
3	109.5	78.8	856	US-11-135-235-1	Sequence 1, Appl
4	104.5	75.2	601	US-11-014-842A-37	Sequence 37, Appl
5	104.5	75.2	613	US-11-014-842A-33	Sequence 33, Appl
6	104.5	75.2	669	US-11-014-842A-29	Sequence 29, Appl
7	104.5	75.2	681	US-11-014-842A-25	Sequence 25, Appl
8	104.5	75.2	789	US-11-014-842A-39	Sequence 39, Appl
9	104.5	75.2	801	US-11-014-842A-35	Sequence 35, Appl
10	104.5	75.2	854	US-11-022-562-219	Sequence 219, Appl
11	104.5	75.2	857	US-11-014-842A-31	Sequence 31, Appl
12	104.5	75.2	869	US-11-014-842A-27	Sequence 27, Appl
13	99.5	71.6	35	US-11-096-725-35	Sequence 35, Appl
14	84	60.4	28	US-11-223-699A-96	Sequence 96, Appl
15	84	60.4	28	US-11-121-566A-96	Sequence 96, Appl
16	84	60.4	30	US-10-923-112A-30	Sequence 30, Appl
17	79	56.8	21	US-11-078-256-288	Sequence 288, Appl
18	79	56.8	27	US-10-985-426-3	Sequence 3, Appl
19	79	56.8	27	US-11-067-092A-11	Sequence 11, Appl
20	79	56.8	27	US-11-016-542-5	Sequence 5, Appl
21	77	55.4	17	US-10-923-112A-29	Sequence 29, Appl
22	77	55.4	17	US-11-223-699A-7	Sequence 7, Appl
23	77	55.4	17	US-11-121-566A-7	Sequence 7, Appl
24	74	53.2	15	US-11-045-024-12977	Sequence 12977, A
25	73.5	52.9	28	US-11-141-725-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-10-510-947-8

Sequence 8, Application US/10510947

Publication No. US20050255123A1

GENERAL INFORMATION:

APPLICANT: The Trustees of the University of Pennsylvania

APPLICANT: Wilson, James M.

APPLICANT: Medina, Maria Fe C.

APPLICANT: Kobinger, Gary

TITLE OF INVENTION: Chimeric Ebola Virus Envelopes and Uses Therefor

FILE REFERENCE: UPN-02811PCT

CURRENT APPLICATION NUMBER: US/10/510,947

CURRENT FILING DATE: 2004-10-28

PRIOR FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/376,480

PRIOR FILING DATE: 2002-06-04

PRIOR APPLICATION NUMBER: US 60/385,704

PRIOR FILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 67

SOFTWARE: PatentIn version 3.2

SEQ ID NO 8

LENGTH: 856

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-10-510-947-8

Query Match 78.8%; Score 109.5; DB 6; Length 856;

Best Local Similarity 82.8%; Pred. No. 5.2e-07;

Matches 24; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Oy 1 AVGMGLAMFLGFLCAAGSTWGATSMALTV 29

Db 512 AVG-IGALFLGFLCAAGSTWGATSMALTV 539

RESULT 2

US-11-042-988-13

Sequence 13, Application US/11042988

Publication No. US20050244818A1

GENERAL INFORMATION:

APPLICANT: SILICIANO, ROBERT

APPLICANT: ZHANG, HAILI

APPLICANT: ZHOU, YAN

TITLE OF INVENTION: SINGLE CELL ANALYSIS OF HIV REPLICATION CAPACITY AND

TITLE OF INVENTION: DRUG RESISTANCE

FILE REFERENCE: 62760(71699)

CURRENT APPLICATION NUMBER: US/11/042,988

Sequence 28, Appl
Sequence 12877, A
Sequence 340, App
Sequence 12943, A
Sequence 12986, A
Sequence 12869, A
Sequence 217, App
Sequence 176, App
Sequence 12980, A
Sequence 948, App
Sequence 950, App
Sequence 8467, Ap
Sequence 951, App
Sequence 8820, Ap
Sequence 947, App
Sequence 8424, Ap
Sequence 817, App
Sequence 8454, Ap
Sequence 949, App
Sequence 8604, Ap

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; CURRENT FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/540,716
; PRIOR FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 13
; LENGTH: 856
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-042-988-13

Query Match      78.8%; Score 109.5; DB 7; Length 856;
Best Local Similarity 82.8%; Pred. No. 5.2e-07;
Matches 24; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTIV 29
Db 512 AVG-IGALFLGFLGAAGSTMGAAASMTLTV 539

RESULT 3
US-11-135-235-1
; Sequence 1, Application US/11135235
; Publication No. US20060019395A1
; GENERAL INFORMATION:
; APPLICANT: Matasco, Wayne
; TITLE OF INVENTION: Lentiviral Vectors and Uses Thereof
; FILE REFERENCE: 20363-027
; CURRENT APPLICATION NUMBER: US/11/135,235
; PRIOR FILING DATE: 2005-05-23
; PRIOR APPLICATION NUMBER: 60/589,610
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 856
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-135-235-1

Query Match      78.8%; Score 109.5; DB 7; Length 856;
Best Local Similarity 82.8%; Pred. No. 5.2e-07;
Matches 24; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTIV 29
Db 512 AVG-IGALFLGFLGAAGSTMGAAASMTLTV 539

RESULT 4
US-11-014-842A-37
; Sequence 37, Application US/11014842A
; Publication No. US20060013826A1
; GENERAL INFORMATION:
; APPLICANT: TANGY, FREDERIC
; APPLICANT: LORIN, CLARISSE
; APPLICANT: MOLLET, LUCILE
; APPLICANT: DELEBEQUE, FREDERIC
; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF
; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
; TITLE OF INVENTION: VACCINE COMPOSITIONS
; FILE REFERENCE: 2356.0093
; CURRENT APPLICATION NUMBER: US/11/014,842A
; CURRENT FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: PCT/EP03/07146
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: EP 02291550.8
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 37
; LENGTH: 601
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
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; ORGANISM: Human immunodeficiency virus type 1
US-11-014-842A-37

Query Match      75.2%; Score 104.5; DB 7; Length 601;
Best Local Similarity 79.3%; Pred. No. 1.6e-06;
Matches 23; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTIV 29
Db 430 AVG-IGAVFLGFLGAAGSTMGAAASVTLTV 457

RESULT 5
US-11-014-842A-33
; Sequence 33, Application US/11014842A
; Publication No. US20060013826A1
; GENERAL INFORMATION:
; APPLICANT: TANGY, FREDERIC
; APPLICANT: LORIN, CLARISSE
; APPLICANT: MOLLET, LUCILE
; APPLICANT: DELEBEQUE, FREDERIC
; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF
; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
; TITLE OF INVENTION: VACCINE COMPOSITIONS
; FILE REFERENCE: 2356.0093
; CURRENT APPLICATION NUMBER: US/11/014,842A
; CURRENT FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: PCT/EP03/07146
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: EP 02291550.8
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 33
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-014-842A-33

Query Match      75.2%; Score 104.5; DB 7; Length 613;
Best Local Similarity 79.3%; Pred. No. 1.6e-06;
Matches 23; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 AVGMGLGAMFLGFLGAAGSTMGATSMALTIV 29
Db 442 AVG-IGAVFLGFLGAAGSTMGAAASVTLTV 469

RESULT 6
US-11-014-842A-29
; Sequence 29, Application US/11014842A
; Publication No. US20060013826A1
; GENERAL INFORMATION:
; APPLICANT: TANGY, FREDERIC
; APPLICANT: LORIN, CLARISSE
; APPLICANT: MOLLET, LUCILE
; APPLICANT: DELEBEQUE, FREDERIC
; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF
; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
; TITLE OF INVENTION: VACCINE COMPOSITIONS
; FILE REFERENCE: 2356.0093
; CURRENT APPLICATION NUMBER: US/11/014,842A
; CURRENT FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: PCT/EP03/07146
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: EP 02291550.8
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 29
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
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US-11-014-842A-29

Query Match 75.2%; Score 104.5; DB 7; Length 669;
Best Local Similarity 79.3%; Pred. No. 1.8e-06;
Matches 23; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 29
||| :||:|||||:|||||:|
Db 498 AVG-IGA VFLGFLGAAGSTMGAASVTLTV 525

RESULT 7

US-11-014-842A-25

; Sequence 25, Application US/11014842A

; Publication No. US20060013826A1

; GENERAL INFORMATION:

; APPLICANT: TANGY, FREDERIC

; APPLICANT: LORIN, CLARISSE

; APPLICANT: MOLLET, LUCILE

; APPLICANT: DELEBEQUE, FREDERIC

; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF

; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF

; TITLE OF INVENTION: VACCINE COMPOSITIONS

; FILE REFERENCE: 2356.0093

; CURRENT APPLICATION NUMBER: US/11/014,842A

; CURRENT FILING DATE: 2004-12-20

; PRIOR APPLICATION NUMBER: PCT/EP03/07146

; PRIOR FILING DATE: 2003-06-20

; PRIOR APPLICATION NUMBER: EP 02291550.8

; PRIOR FILING DATE: 2002-06-20

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 25

; LENGTH: 681

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

US-11-014-842A-25

Query Match 75.2%; Score 104.5; DB 7; Length 681;
Best Local Similarity 79.3%; Pred. No. 1.8e-06;
Matches 23; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 29
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Db 510 AVG-IGA VFLGFLGAAGSTMGAASVTLTV 537

RESULT 8

US-11-014-842A-39

; Sequence 39, Application US/11014842A

; Publication No. US20060013826A1

; GENERAL INFORMATION:

; APPLICANT: TANGY, FREDERIC

; APPLICANT: LORIN, CLARISSE

; APPLICANT: MOLLET, LUCILE

; APPLICANT: DELEBEQUE, FREDERIC

; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF

; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF

; TITLE OF INVENTION: VACCINE COMPOSITIONS

; FILE REFERENCE: 2356.0093

; CURRENT APPLICATION NUMBER: US/11/014,842A

; CURRENT FILING DATE: 2004-12-20

; PRIOR APPLICATION NUMBER: PCT/EP03/07146

; PRIOR FILING DATE: 2003-06-20

; PRIOR APPLICATION NUMBER: EP 02291550.8

; PRIOR FILING DATE: 2002-06-20

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 39

; LENGTH: 789

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

US-11-014-842A-39

Query Match 75.2%; Score 104.5; DB 7; Length 854;
Best Local Similarity 79.3%; Pred. No. 2.4e-06;
Matches 23; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Query Match 75.2%; Score 104.5; DB 7; Length 789;
Best Local Similarity 79.3%; Pred. No. 2.2e-06;
Matches 23; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 29
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Db 430 AVG-IGA VFLGFLGAAGSTMGAASVTLTV 457

RESULT 9

US-11-014-842A-35

; Sequence 35, Application US/11014842A

; Publication No. US20060013826A1

; GENERAL INFORMATION:

; APPLICANT: TANGY, FREDERIC

; APPLICANT: LORIN, CLARISSE

; APPLICANT: MOLLET, LUCILE

; APPLICANT: DELEBEQUE, FREDERIC

; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF

; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF

; TITLE OF INVENTION: VACCINE COMPOSITIONS

; FILE REFERENCE: 2356.0093

; CURRENT APPLICATION NUMBER: US/11/014,842A

; CURRENT FILING DATE: 2004-12-20

; PRIOR APPLICATION NUMBER: PCT/EP03/07146

; PRIOR FILING DATE: 2003-06-20

; PRIOR APPLICATION NUMBER: EP 02291550.8

; PRIOR FILING DATE: 2002-06-20

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 35

; LENGTH: 801

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

US-11-014-842A-35

Query Match 75.2%; Score 104.5; DB 7; Length 801;
Best Local Similarity 79.3%; Pred. No. 2.2e-06;
Matches 23; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 AVGMGLGAMFLGFLGAAGSTMGTSMALTV 29
||| :||:|||||:|||||:|
Db 442 AVG-IGA VFLGFLGAAGSTMGAASVTLTV 469

RESULT 10

US-11-022-562-219

; Sequence 219, Application US/11022562

; Publication No. US20050249742A1

; GENERAL INFORMATION:

; APPLICANT: Ruprecht, Ruth M.

; APPLICANT: Shisong, Jiang

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING

; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE

; FILE REFERENCE: DFN-043CN

; CURRENT APPLICATION NUMBER: US/11/022,562

; CURRENT FILING DATE: 2004-12-22

; PRIOR APPLICATION NUMBER: PCT/US03/20322

; PRIOR FILING DATE: 2003-06-27

; PRIOR APPLICATION NUMBER: 60/392718

; PRIOR FILING DATE: 2002-06-27

; NUMBER OF SEQ ID NOS: 340

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 219

; LENGTH: 854

; TYPE: PRT

; ORGANISM: Human Immunodeficiency Virus

US-11-022-562-219

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-223-699A-96

Query Match 60.4%; Score 84; DB 7; Length 28;
Best Local Similarity 89.5%; Pred. No. 2.6e-05;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GAMFLGFLGAAGSTMGATS 24
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Db 1 GAFGLGFLGAAGSTMGAWS 19

RESULT 15

US-11-121-566A-96
; Sequence 96, Application US/11121566A
; Publication No. US20060040882A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, LISHAN
; APPLICANT: CUI, KUNYUAN
; APPLICANT: CHEN, YUCHENG
; APPLICANT: MAYER, SASHA
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENHANCING DELIVERY OF
; TITLE OF INVENTION: NUCLEIC ACIDS INTO CELLS AND FOR MODIFYING EXPRESSION
; TITLE OF INVENTION: OF TARGET GENES IN CELLS
; FILE REFERENCE: 04-0305
; CURRENT APPLICATION NUMBER: US/11/121.566A
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/667,833
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/656,572
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 60/613,416
; PRIOR FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/570,513
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/570,512
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/568,027
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 96
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-11-121-566A-96

Query Match 60.4%; Score 84; DB 7; Length 28;
Best Local Similarity 89.5%; Pred. No. 2.6e-05;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GAMFLGFLGAAGSTMGATS 24
||:|||||
Db 1 GAFGLGFLGAAGSTMGAWS 19

Search completed: March 7, 2006, 17:57:11
Job time : 2.11209 secs

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GenCore version 5.1.7
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Run on: March 7, 2006, 17:40:32 ; Search time 262.28 Seconds
(without alignments)
1087.222 Million cell updates/sec

Title: US-09-938-406-1_COPY_33_681
Perfect score: 3474

Sequence: 1 ANLWVTVYGVVWKEATTT.....ONQOEKQQLQLDKWASL 649

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	2987	86.0	862	9 AEB10584	Aeb10584 Clade B e
4	2977.5	85.7	883	4 AAB82761	Aab82761 Ancestral
5	2977.5	85.7	883	9 ADW38347	Adw38347 Ancestral
6	2977.5	85.7	883	9 ADY27998	Ady27998 HIV-1 gro
7	2977.5	85.7	883	9 AEB10654	Aeb10654 ANI-EnvB
8	2977.5	85.7	883	9 AEB10552	Aeb10552 HIV-1, su
9	2970	85.5	850	9 ADZ07749	Adz07749 HIV subty
10	2949	84.9	862	9 AEB10583	Aeb10583 Clade B e
11	2947	84.8	842	9 ADY99903	Ady99903 Human cod
12	2947	84.8	1068	9 ADY99925	Ady99925 Human cod
13	2947	84.8	2602	9 ADY99929	Ady99929 Human cod
14	2939.5	84.6	841	9 ADZ07752	Adz07752 HIV CON-B
15	2937.5	84.3	841	9 ADZ07794	Adz07794 HIV CON-B
16	2922	84.1	840	9 ADZ07797	Adz07797 HIV B anc
17	2891.5	83.2	856	6 ABR55495	Abr55495 Amino aci
18	2883.5	83.0	842	6 ABR55684	Abr55684 HIV isola
19	2883.5	83.0	842	7 ADC13218	Adc13218 Protein o
20	2883.5	83.0	842	9 ADW48030	Adw48030 HIV strai
21	2883.5	83.0	847	3 AAY97073	Aay97073 Variant H
22	2883.5	83.0	847	8 ADO05103	Ado05103 Human imm
23	2883.5	83.0	847	9 ADZ82338	Adz82338 HIV-1 pol
24	2878.5	82.9	842	6 ABU66565	Abu66565 Human imm

25	2876.5	82.8	842	8 ADM73868	Adm73868 HIV-1 pol
26	2870.5	82.6	842	5 ABB06211	Abb06211 HIV Env 1
27	2869.5	82.6	843	9 ADX39692	Adx39692 HIV Env p
28	2867.5	82.5	842	9 ADZ04164	Adz04164 Env prote
29	2852	82.1	850	2 AAR67724	Aar67724 gp120 fro
30	2849.5	82.0	847	8 ADK14406	Adk14406 HIV wild-
31	2849.5	82.0	847	8 ADP20081	Adp20081 Human imm
32	2845.5	81.9	847	8 ADK14404	Adk14404 HIV mutan
33	2845	81.9	856	9 ADX39677	Adx39677 HIV Env p
34	2844	81.9	856	9 ADX39681	Adx39681 HIV Env p
35	2843.5	81.9	847	8 ADK14405	Adk14405 HIV mutan
36	2840.5	81.8	791	9 ADX39690	Adx39690 HIV Env p
37	2836.5	81.6	855	9 ADX39676	Adx39676 HIV Env p
38	2834	81.6	855	2 AAW11581	Aaw11581 Human imm
39	2834	81.6	855	2 AAW88113	Aaw88113 Env prote
40	2831.5	81.5	855	9 ADX39674	Adx39674 HIV Env p
41	2827.5	81.4	643	4 AAB61505	Aab61505 HIV-1 SOS
42	2827.5	81.4	643	6 ABR57052	Abr57052 HIV-1 JR-
43	2827.5	81.4	643	7 ADF18107	Adf18107 HIV-1 JR-
44	2827.5	81.4	643	8 ADK14399	Adk14399 HIV gp140
45	2827.5	81.4	643	8 ADU22853	Adu22853 HIV-1 JR-

ALIGNMENTS

RESULT 1

AAW44250	
ID	AAW44250 standard; protein; 649 AA.
XX	
AC	AAW44250;
XX	
DT	17-OCT-2003 (revised)
DT	26-JUN-1998 (first entry)
XX	
DE	HIV-1 gp160 residues 33-681.
XX	
KW	Vaccine; antibody; antigen; hydrophobic; proteosome; pathogen;
KW	immune response; sexually transmitted disease; HIV; infection.
XX	
OS	Human immunodeficiency virus 1.
XX	
PH	Key Location/Qualifiers
FT	Region 491..519
FT	/note="hydrophobic region"
XX	
PN	WO9801558-A2.
XX	
PD	15-JAN-1998.
XX	
PF	10-JUL-1997; 97MO-US012253.
XX	
PR	10-JUL-1996; 96US-0021687P.
XX	
PA	(INTE-) INTELLIVAX INC.
PA	(JACK-) JACKSON FOUND HENRY M.
PA	(USSA) US SEC OF ARMY.
XX	
PI	Lowell GH, Vancott TC, Birx DL;
XX	
DR	WPI; 1998-110231/10.
XX	

Vaccine compositions for eliciting neutralising antibodies - comprising antigen containing hydrophobic sequence or having added hydrophobic material, complexed to proteosomes or bio-adhesive nano-emulsions.

Claim 9; Page 22; 62pp; English.

The present sequence represents HIV-1 gp160 residues 33-681 (the full protein is on the SWISS-PROT database Seq ID: 119434) used in a vaccine of the present invention. The vaccine composition is capable of eliciting neutralising antibodies in a subject to a pathogenic organism which antibodies are present in vaginal secretions, intestinal secretions, lung

Db 92 FMWKNMVEQMHEDIISLDQSLKPCVKLTPLCVTLNCTDAN-KVATNTNTHSSS-----GG 146
Qy 122 QRGKGMENCSFNITTSIRDKVQREYALFYKLDVEPIDDNKNTNTNTKYRLINCNTSVIT 181
Db 147 TWEKGMKNCFSNITTSIRDKVQREYALFYKLDVVPIDNNDNNNTNRYRLINCNTSVIT 206
Qy 182 QACPVSFEPIPIHYCTPTGALLKNDKNGTGCTNVSTVQCTHGIRPVSTQLLN 241
Db 207 QACPVSFEPIPIHYCTPTGALLKNDKNGTGCTNVSTVQCTHGIRPVSTQLLN 266
Qy 242 GSIAEEVVRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPRVWYTTGAIL 301
Db 267 GSIAEEVVRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPRVWYTTGAIL 326
Qy 302 GNIRAHNCISRAQWNTLQIATTLREQFG-NKTIAFNQSSGGDPEIVMHSFNCGGEFF 360
Db 327 GDIRAHNCISRAQWNTLQIATTLREQFG-NKTIAFNQSSGGDPEIVMHSFNCGGEFF 386
Qy 361 YCNSTQLFNSAWNTSNGTWSVTRKQKDTGDIITLPCRILKQIINRWQVGMAYALPIKG 420
Db 387 YCNSTQLFNSAWNTSNGTWSVTRKQKDTGDIITLPCRILKQIINRWQVGMAYALPIKG 445
Qy 421 LIRCSNITGLLLTRDGGENOT--TEIFRPGGDMRDNWRSELKYKVKVIEPLGVAPT 478
Db 446 QIKCSNITGLLLTRDGGENOT--TEIFRPGGDMRDNWRSELKYKVKVIEPLGVAPT 504
Qy 479 KAKRVRQREKRAVGMGLGAMFLGFLGAGSTMGATSMALTVOARQLLSGIVQQNNLLRA 538
Db 505 KAKRVRQREKRAVGMGLGAMFLGFLGAGSTMGATSMALTVOARQLLSGIVQQNNLLRA 564
Qy 539 IKAQHLLQLTWGILKQIARILAVERYLKQDLGFGWCSGKLICTTAVPWNASWNT 598
Db 565 IEAQHLLQLTWGILKQIARILAVERYLKQDLGFGWCSGKLICTTAVPWNASWNT 624
Qy 599 LDOIWNNTWMEDEIDNTHLYTLIESNQKQEQELLQDLKWSL 649
Db 625 LDKIWNNTWMEDEIDNTHLYTLIESNQKQEQELLQDLKWSL 675
RESULT 11
ADY99903
ID ADY99903 standard; protein; 842 AA.
XX AC ADY99903;
DT 16-JUN-2005 (first entry)
XX DE Human codon-optimized HIV B Env protein.
XX KW env; viral replication; recombinant DNA; vector; vaccine; cancer;
KW infectious disease; HIV; hepatitis; varicella virus infection;
KW immune stimulation; antimicrobial; virucide; anti-HIV; cytostatic;
KW antinflammatory; hepatotropic; immunogenicity.
XX OS Homo sapiens.
OS OS Human immunodeficiency virus 1.
XX PN WO2005028634-A2.
XX PD 31-MAR-2005.
XX PF 20-SEP-2004; 2004WO-US030849.
XX PR 18-SEP-2003; 2003US-0504030P.
XX PA (UYEM-) UNIV EMORY.
XX PI Feinberg MMD, Garber D;
XX WPI; 2005-254126/26.
XX DR N-PSDB; ADY99902.
XX PT New recombinant modified vaccinia Ankara virus comprising first null

PT mutation in vaccinia gene, useful for treating or preventing viral
PT infection (e.g. HIV, hepatitis and smallpox), and cancer.
XX Claim 69; SEQ ID NO 31; 324pp; English.
XX This invention relates to a novel recombinant modified vaccinia Ankara
CC virus (rMVA). Specifically, it refers to the use of rMVA vectors in the
CC development of vaccines to protect against cancer or infectious viral
CC diseases such as HIV, hepatitis and smallpox. The present invention
CC describes introducing a null mutation (preferably a deletion) into a
CC vaccinia gene that is necessary for replication of the rMVA, in
CC particular an exemplary gene is the vaccinia uracil DNA glycosylase gene.
CC Additional vaccinia genes that can contain null mutations include, but
CC are not limited to, I11 beta receptor, A46R, IL-18BP, A41L and E3L.
CC Accordingly, it provides a system for producing an appropriate vaccine
CC that involves an immortalized, non-transformed avian fibroblast cell
CC infected with the rMVA, where the cell is from a complementing cell line
CC that is engineered to express the gene necessary for viral replication,
CC such that the virus is able to propagate. Furthermore, the rMVA may
CC include a heterologous nucleic acid sequence encoding an antigen or a
CC fragment thereof derived from viral, animal or plant polynucleotides, for
CC example this may include an antigen from the HIV virus, measles virus,
CC SARS virus, influenza virus, malaria plasmodium, tuberculosis bacillus,
CC yellow fever virus, dengue flavivirus or the river blindness nematode.
CC The rMVA also comprises a second heterologous nucleic acid sequence
CC encoding a pro-apoptotic, anti-apoptotic or an immunomodulator operably
CC linked to an early stage viral promoter. As such, the developed vaccine
CC can be administered in a sufficient amount to effect an immune response
CC in a host and exhibits antimicrobial, virucide, anti-HIV, cytostatic,
CC antinflammatory and hepatotropic activities. This polypeptide sequence
CC is a human codon-optimized HIV-1 consensus protein sequence, encoded by
CC an antigenic sequence of an MVA-based vector given in an exemplification
CC of the invention.
XX SQ Sequence 842 AA;
Query Match 84.8%; Score 2947; DB 9; Length 842;
Beat Local Similarity 86.2%; Pred. No. 5.4e-158;
Matches 558; Conservative 25; Mismatches 4; Indels 24; Gaps 5;
Qy 3 LMTVYVYGVVWKEATTTLCASDAKAYDTAHNVWATHACVPTNPQEVVLENTNF 62
Db 33 LMTVYVYGVVWKEATTTLCASDAKAYDTAHNVWATHACVPTNPQEVVLENTNF 92
Qy 63 NNMKNMVEQMHEDIISLDQSLKPCVKLTPLCVTLNCTDNLNNTNTTNTLSIIVWREQ 122
Db 93 NNMKNMVEQMHEDIISLDQSLKPCVKLTPLCVTLNCTDNLNNTNTSSS---NET 146
Qy 123 RKGEMRNCFSNITTSIRDKVQREYALFYKLDVEPIDDNKNTNTKYRLINCNTSVITQ 182
Db 147 MEKGEIKNCFSNITTSIRDKVQREYALFYKLDVVPID-----NAYRLISCNTSVITQ 199
Qy 183 ACPKVSFEPIPIHYCTPTGALLKNDKNGTGCTNVSTVQCTHGIRPVSTQLLN 242
Db 200 ACPKVSFEPIPIHYCAPAGFAILLKNDKNGTGCTNVSTVQCTHGIRPVSTQLLN 259
Qy 243 SLAEEVVRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPRVWYTTGAIL 302
Db 260 SLAEEVVRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPRVWYTTGAIL 319
Qy 303 NIQAHCNISRAQWNTLQIATTLREQFG-NKTIAFNQSSGGDPEIVMHSFNCGGEFFVC 362
Db 320 DIRAHNCISRAQWNTLQIATTLREQFG-NKTIAFNQSSGGDPEIVMHSFNCGGEFFVC 379
Qy 363 NSTQLFNSAWNTSNGTWSVTRKQKDTGDIITLPCRILKQIINRWQVGMAYALPIKGLI 422
Db 380 NSTQLF-----TNWTRKLNNTGNITLPCRILKQIINRWQVGMAYALPIKGLI 429
Qy 423 RCSSNITGLLLTRDGGENOTTEIFRPGGDMRDNWRSELKYKVKVIEPLGVAPTAKR 482
Db 430 RCSSNITGLLLTRDGGENOTTEIFRPGGDMRDNWRSELKYKVKVIEPLGVAPTAKR 489
Qy 483 RVVQREKRAVGMGLGAMFLGFLGAGSTMGATSMALTVOARQLLSGIVQQNNLLRAIKAQ 542

Db 490 RVVQREKRAVG-IGAMFLGFLGAAGSTWGAASMTLTVOARQLLSGIVQQNNLLRAIEAQ 548
 QY 543 QHLLQLTWGKIQLOARILAVERYLKDQQLLGFWCGSGKLICTTAVPWNASWSNKTLDQI 602
 Db 549 QHLLQLTWGKIQLOARVLAVERYLKDQQLLGFWCGSGKLICTTAVPWNASWSNKTLDQI 608
 QY 603 WNNMTWMEWDREIDNYTHLYLTIIEESQNOQKQOELLQLDKWASL 649
 Db 609 WNNMTWMEWEREIDNYTSLIYTIIEESQNOQKQOELLQLDKWASL 655

RESULT 12

ADY99925
 ID ADY99925 standard; protein; 1068 AA.

XX AC ADY99925;

XX DT 16-JUN-2005 (first entry)

XX DE Human codon-optimized HIV B Env-Nef fusion protein.

XX KW env; nef; fusion protein; viral replication; recombinant DNA; vector;
 KW vaccine; cancer; infectious disease; HIV; hepatitis;
 KW variola virus infection; immune stimulation; antimicrobial; virucide;
 KW anti-HIV; cytostatic; antiinflammatory; hepatotropic; immunogenicity.

XX OS Homo sapiens.

XX OS Human immunodeficiency virus 1.

XX PN WO2005028634-A2.

XX PD 31-MAR-2005.

XX PF 20-SEP-2004; 2004WO-US030849.

XX PR 18-SEP-2003; 2003US-0504030P.

XX PA (UYEM-) UNIV EMORY.

XX PI Feinberg MMD, Garber D;

XX DR WPI; 2005-254126/26.

XX DR N-PSDB; ADY99924.

XX PT New recombinant modified vaccinia Ankara virus comprising first null
 PT mutation in vaccinia gene, useful for treating or preventing viral
 PT infection (e.g. HIV, hepatitis and smallpox), and cancer.

XX PS Claim 69; SEQ ID NO 53; 324pp; English.

XX CC This invention relates to a novel recombinant modified vaccinia Ankara
 CC virus (rMVA). Specifically, it refers to the use of rMVA vectors in the
 CC development of vaccines to protect against cancer or infectious viral
 CC diseases such as HIV, hepatitis and smallpox. The present invention
 CC describes introducing a null mutation (preferably a deletion) into a
 CC vaccinia gene that is necessary for replication of the rMVA, in
 CC particular an exemplary gene is the vaccinia uracil DNA glycosylase gene.
 CC Additional vaccinia genes that can contain null mutations include, but
 CC are not limited to, IL1 beta receptor, A46R, IL-18BP, A41L and E3L.
 CC Accordingly, it provides a system for producing an appropriate vaccine
 CC that involves an immortalized, non-transformed avian fibroblast cell
 CC infected with the rMVA, where the cell is from a complementing cell line
 CC that is engineered to express the gene necessary for viral replication,
 CC such that the virus is able to propagate. Furthermore, the rMVA may
 CC include a heterologous nucleic acid sequence encoding an antigen or a
 CC fragment thereof derived from viral, animal or plant polynucleotides, for
 CC example this may include an antigen from the HIV virus, measles virus,
 CC SARS virus, influenza virus, malaria plasmodium, tuberculosis Bacillus,
 CC yellow fever virus, dengue flavivirus or the river blindness nematode.
 CC The rMVA also comprises a second heterologous nucleic acid sequence
 CC encoding a pro-apoptotic, anti-apoptotic or an immunomodulator operably
 CC linked to an early stage viral promoter. As such, the developed vaccine

CC can be administered in a sufficient amount to effect an immune response
 CC in a host and exhibits antimicrobial, virucide, anti-HIV, cytostatic,
 CC antiinflammatory and hepatotropic activities. This polypeptide sequence
 CC is a human codon-optimized HIV-1 consensus fusion protein sequence,
 CC encoded by an antigenic sequence of an MVA-based vector given in an
 CC exemplification of the invention.

XX SQ Sequence 1068 AA;

Query Match 84.8%; Score 2947; DB 9; Length 1068;
 Best Local Similarity 86.2%; Pred. No. 6.6e-158;
 Matches 558; Conservative 25; Mismatches 40; Indels 24; Gaps 5;

QY 3 LWTVTYGVVPWKKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQSVLENVTENF 62

Db 33 LWTVTYGVVPWKKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQSVLENVTENF 92

QY 63 NMWKNNVVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTTSTLSIIVWEQ 122

Db 93 NMWKNNVVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTTSSS---WET 146

QY 123 RGKGMNCSFNITTSIRDVQREYALFYKLDVEPIDDNKNNTNTKYRLINCNTSVITQ 182

Db 147 MEKGEIKNCSFNITTSIRDVQREYALFYKLDVVPID-----NASYRLISCNTSVITQ 199

QY 183 ACPKVSEPIPIHYCTPTGALLKCNDDKENGTPCTNVSTVQCTHGIRVWSTQLLNG 242

Db 200 ACPKVSEPIPIHYCAPAGFAILLKCNDDKFNCTNVSTVQCTHGIRVWSTQLLNG 259

QY 243 SLAEVEVIRSENFTNNAKTIIVQLNVSVINCTRNPNHTRKRVTLQPGVWVTTGILG 302

Db 260 SLAEVEVIRSENFTNNAKTIIVQLNVSVINCTRNPNHTRKRVTLQPGVWVTTGILG 319

QY 303 NIRQAHCNISRAQNNNTLQOIATTLREQFNKNTAFNQSSGGDPEIVMHSFNCGGEFFYC 362

Db 320 DIRQAHCNISRAQNNNTLQOIVIKLREQFNKNTAFNQSSGGDPEIVMHSFNCGGEFFYC 379

QY 363 NSTOLFNSANWVTSNGTWSVTRKQKDTGDIITLPCRIKOIINRWQVVKAMYPKGLI 422

Db 380 NSTOLF-----TWNDTRKLNNTGRNITLPCRIKOIINRWQVVKAMYPKGLI 429

QY 423 RCSSNITGLLLTRDGGGNOTTEIFRPGGDMNDRSELYKYVKVKEPLGVAPTKAKR 482

Db 430 RCSSNITGLLLTRDGGGNOTTEIFRPGGDMNDRSELYKYVKVKEPLGVAPTKAKR 489

QY 483 RVVQREKRAVGMIGAMFLGFLGAAGSTWGAASMTLTVOARQLLSGIVQQNNLLRAIEAQ 542

Db 490 RVVQREKRAVG-IGAMFLGFLGAAGSTWGAASMTLTVOARQLLSGIVQQNNLLRAIEAQ 548

QY 543 QHLLQLTWGKIQLOARILAVERYLKDQQLLGFWCGSGKLICTTAVPWNASWSNKTLDQI 602

Db 549 QHLLQLTWGKIQLOARVLAVERYLKDQQLLGFWCGSGKLICTTAVPWNASWSNKTLDQI 608

QY 603 WNNMTWMEWDREIDNYTHLYLTIIEESQNOQKQOELLQLDKWASL 649

Db 609 WNNMTWMEWEREIDNYTSLIYTIIEESQNOQKQOELLQLDKWASL 655

RESULT 13

ADY99929

ID ADY99929 standard; protein; 2602 AA.

XX AC ADY99929;

XX DT 16-JUN-2005 (first entry)

XX DE Human codon-optimized HIV B Gag-Pol-Env-Nef fusion protein.

XX KW gag; pol; env; nef; fusion protein; viral replication; recombinant DNA;
 KW vector; vaccine; cancer; infectious disease; HIV; hepatitis;
 KW variola virus infection; immune stimulation; antimicrobial; virucide;
 KW anti-HIV; cytostatic; antiinflammatory; hepatotropic; immunogenicity.

PS Disclosure; Fig 28A; 284pp; English.

XX The invention describes an isolated protein (I) selected from 106 fully defined 500-866 amino acid sequences given in the specification. Also described are: a nucleic acid comprising: a nucleotide sequence encoding CON6 HIV gp160 protein, subtype C ancestral HIV envelope protein, subtype C consensus HIV envelope protein, subtype C consensus HIV gag protein, subtype A consensus HIV envelope protein, Group M consensus HIV gag protein, subtype A consensus HIV pol protein, Group M consensus HIV nef protein, subtype C consensus HIV pol protein, subtype B consensus HIV gag protein, or subtype B consensus HIV envelope protein, where the nucleotide sequence comprises codons optimized for expression in human cells; a nucleotide sequence encoding (I); or a nucleotide sequence selected from 89 fully defined 633-2607 bp sequences given in the specification; a vector comprising the nucleic acid of (1); a composition comprising at least one protein or nucleic acid above and a carrier; and inducing an immune response in a mammal. The protein is a consensus or ancestral immunogen useful for inducing antibodies that neutralize a wide spectrum of HIV primary isolates and/or that induces a T cell response. This is the amino acid sequence of a HIV (CON-B) consensus gp140 env fusion protein.

XX Sequence 841 AA;

Query Match 84.6%; Score 2939.5; DB 9; Length 841;

Best Local Similarity 86.1%; Pred. No. 1.4e-157;

Matches 557; Conservative 31; Mismatches 34; Indels 25; Gaps 7;

Qy 3 LWTVVYGVVWKEATTLFCASDAKAYDTFAHNVWATHACVTPNPNPQEVLENVTENF 62

Db 33 LWTVVYGVVWKEATTLFCASDAKAYDTFAHNVWATHACVTPNPNPQEVLENVTENF 92

Qy 63 NMWKNVVEQHEHDIISLWDSLKPCVKLTPLCVTLNCTDLNNTNTTSLIIVWVEQ 122

Db 93 NMWKNVVEQHEHDIISLWDSLKPCVKLTPLCVTLNCTDLNNTNTT---IYRW-- 147

Qy 123 RGKGMENCSFNITTSIRDKVOREYALFYKLDVPEIDDKNTNTNTYRLINCNTSVITQ 182

Db 148 --RGEIKNCNSFNITTSIRDKVOREYALFYKLDVPEIDN-----DNTSYRLINCNTSVITQ 200

Qy 183 ACPKVSPEPIPIHYCTPTGFALLKNDKFKNGTGTCTNVTSTVQCTHGIRPVSTQLLNG 242

Db 201 ACPKVSPEPIPIHYCAPAGPAILKNDKFKNGTGTCTNVTSTVQCTHGIRPVSTQLLNG 260

Qy 243 SLAEVIVRSNTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGILG 302

Db 261 SLAEVIVRSNTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGILG 320

Qy 303 NIRAQHCNISRAQNNWTLQIATTLRQFGNKTIAFNQSGGDPDEIIVMHSFNCGGFFYC 362

Db 321 DIRAHCNISRAQNNWTLQIATTLRQFGNKTIVFNQSGGDPDEIIVMHSFNCGGFFYC 380

Qy 363 NSTQFNLSAMNVTSTNGTSTVRKQKTDGIITLPCRIKQIINRWQVVGKAMYPKIGLI 422

Db 381 NTTQLFNSTW---NGTWN-----NTEGNTLPCRIKQIINRWQVVGKAMYPKIGLI 430

Qy 423 RCSSNITGLLTRGGGNGQTEIFRPGGDMRNWSELYKYKVKIEPLGVAPTAKR 482

Db 431 RCSSNITGLLTRDGG--NNETEIFRPGGDMRNWSELYKYKVKIEPLGVAPTAKR 488

Qy 483 RVVQREKRVGMLGAMFLGFLGAAGSTWGATSMALTVOARQLLSGIYQQNNLLRAKQ 542

Db 489 RVVQREKRVG-IGAMFLGFLGAAGSTWGATSMALTVOARQLLSGIYQQNNLLRAKQ 547

Qy 543 QHLLQLTWGIGKQLQARILAVERYLKDQLLGFQCSGKLICTTAVPWNASWSNKLDDQI 602

Db 548 QHLLQLTWGIGKQLQARVILAVERYLKDQLLGFQCSGKLICTTAVPWNASWSNKLDDQI 607

Qy 603 WNNWTWEDREINDYTHLIVTLTEESQNOEKQKQELLQDKWASL 649

Db 608 WDNWTWEDREINDYTHLIVTLTEESQNOEKQKQELLQDKWASL 654

RESULT 15

ADZ07794

ID ADZ07794 standard; protein; 841 AA.

XX AC ADZ07794;

DT 16-JUN-2005 (first entry)

DE HIV CON-B env protein.

XX anti-HIV; Immunostimulant; immune stimulation; HIV infection; infection;

KW CON-B; env; envelope.

XX Human immunodeficiency virus.

XX WO2005028625-A2.

XX 31-MAR-2005.

XX 17-SEP-2004; 2004WO-US030397.

XX 17-SEP-2003; 2003US-0503460P.

XX 27-AUG-2004; 2004US-0604722P.

XX (UYDU-) UNIV DUKE.

XX (KORB/) KORBER B T.

XX (HAHV/) HAHN B H.

XX (SHAW/) SHAW G M.

XX (KOTH/) KOTHE D.

XX (LIYV/) LI Y Y.

XX (DECK/) DECKER J.

PI Korber BT, Hahn BH, Shaw GM, Kothe D, Li YY, Decker J;

PI Haynes BF, Gao F, Liao H;

XX WPI; 2005-242571/25.

XX N-PSDB; ADZ07796.

PT New isolated consensus or ancestral immunogenic proteins, useful for

PT inducing antibodies that neutralize a wide spectrum of human

PT immunodeficiency virus (HIV) primary isolates and/or that induces a T

XX cell response.

XX Claim 66; Fig 44A; 284pp; English.

CC The invention describes an isolated protein (I) selected from 106 fully

CC defined 500-866 amino acid sequences given in the specification. Also

CC described are: a nucleic acid comprising: a nucleotide sequence encoding

CC CON6 HIV gp160 protein, subtype C ancestral HIV envelope protein, subtype

CC C consensus HIV envelope protein, subtype C consensus HIV gag protein,

CC subtype C consensus HIV nef protein, Group M consensus HIV envelope

CC protein, subtype A consensus HIV envelope protein, Group M consensus HIV

CC gag protein, Group M consensus HIV pol protein, Group M consensus HIV nef

CC protein, subtype C consensus HIV pol protein, subtype B consensus HIV gag

CC protein, or subtype B consensus HIV envelope protein, where the

CC nucleotide sequence comprises codons optimized for expression in human

CC cells; a nucleotide sequence encoding (I); or a nucleotide sequence

CC selected from 89 fully defined 633-2607 bp sequences given in the

CC specification; a vector comprising the nucleic acid of (1); a composition

CC comprising at least one protein or nucleic acid above and a carrier; and

CC inducing an immune response in a mammal. The protein is a consensus or

CC ancestral immunogen useful for inducing antibodies that neutralize a wide

CC spectrum of HIV primary isolates and/or that induces a T cell response.

CC This is the amino acid sequence of HIV (CON-B) env protein.

XX Sequence 841 AA;

Query Match 84.3%; Score 2927.5; DB 9; Length 841;

Best Local Similarity 85.9%; Pred. No. 6.8e-157;

Matches 556; Conservative 31; Mismatches 35; Indels 25; Gaps 7;

Qy 3 LWTVVYGVVWKEATTLFCASDAKAYDTFAHNVWATHACVTPNPNPQEVLENVTENF 62

Db 33 L W V Y Y G V P W K E A T T L F G A S D A K A Y D T E V H N W A H A C V P T D P N P Q E V L E N V T E N F 92
Qy 63 N M W K N M V E Q M H E D I I S L W D Q S L K P C V K L T P L C V T L N C T D L N T N T T N T T E L S I I V V W E Q 122
Db 93 N M W K N M V E Q M H E D I I S L W D Q S L K P C V K L T P L C V T L N C T D L N T N T T N T T E L S I I V V W E Q 147
Qy 123 R G K G M R N C S F N I T T S I R D K V Q R E Y A L F Y K L D V E P I D D N K N T N T N T K Y R L N C N T S V I T Q 182
Db 148 -- R G E I K N C S F N I T T S I R D K V Q R E Y A L F Y K L D V E P I D N --- D N T S Y R L I S C N T S V I T Q 200
Qy 183 A C P K V S F E P I P I H Y C T P T G F A L L K N D K F N G T G C T N V S T V Q C T H G I R P V V T T O L L I N G 242
Db 201 A C P K V S F E P I P I H Y C A P A G A I L K N D K F N G T G C T N V S T V Q C T H G I R P V V T T O L L I N G 260
Qy 243 S L A E E V I R S E N F T N A K T I I V Q L N V S V E I N C T R P N N H R K R V T L G P R V M Y T T G E I L G 302
Db 261 S L A E E V I R S E N F T N A K T I I V Q L N V S V E I N C T R P N N H R K R V T L G P R V M Y T T G E I L G 320
Qy 303 N I R O A H C N I S R A Q W N T L Q O I A T T L R E Q F G N K T I A F N Q S S G D P E I V M H S F N C G G E P F Y C 362
Db 321 D I R O A H C N I S R A Q W N T L Q O I A T T L R E Q F G N K T I A F N Q S S G D P E I V M H S F N C G G E P F Y C 380
Qy 363 N S T O L F N G A W N V T S N G T W S V T R K Q D T G D I I T L P C R I K O I I N R M O V G K A M Y A L P I K G I J 422
Db 381 N T T Q L F N S T W --- N G T W N --- N T E G N I T L P C R I K O I I N R M O V G K A M Y A L P I K G I J 430
Qy 423 R C S S N I T G L L T R D G G E N Q T T E I F R P G G D M R D N R S E L Y K Y K V K I E P L G V A P T K A R 482
Db 431 R C S S N I T G L L T R D G G -- N N E T E I F R P G G D M R D N R S E L Y K Y K V K I E P L G V A P T K A R 488
Qy 483 R V V Q R E K R A V G M L G A M F L G F L G A G S T W G A T S M A L T V O A R O L L S G I V O Q O N N L L R A I K A Q 542
Db 489 R V V Q R E K R A V G -- I G A M F L G F L G A G S T W G A A S M T L T V O A R O L L S G I V O Q O N N L L R A I E A Q 547
Qy 543 Q H L L Q L T V W G I K O L Q A R I L A V E R Y L K D O Q L L G F W C S G K L I C T T A P W N A S W S N K T L D O I 602
Db 548 Q H L L Q L T V W G I K O L Q A R I L A V E R Y L K D O Q L L G I W C S G K L I C T T A P W N A S W S N K S L D E I 607
Qy 603 W N N T M W E W R E I D N Y T L I Y T L I E S Q N Q E K N Q O E L L Q L D K W A S L 649
Db 608 W D N T M W E W E R E I D N Y T L I Y T L I E S Q N Q E K N Q O E L L E L D K W A S L 654

Search completed: March 7, 2006, 17:45:23
Job time : 268.28 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: March 7, 2006, 17:45:48 ; Search time 49.7758 Seconds
(without alignments)
1254.519 Million cell updates/sec
Title: US-09-938-406-1_COPY_33_681
Perfect score: 3474
Sequence: 1 ANLWVTYVYGVVWKEATT.....NQQEKQOELLQLDKWASL 649
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR 80:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3474	100.0	868	1 VCLJH4	env polyprotein -
2	2869.5	82.6	843	1 H44001	env polyprotein pr
3	2858	82.3	856	1 VCLJ3W	env polyprotein pr
4	2849.5	82.0	847	2 T09448	envelope glycoprot
5	2837	81.7	852	2 T12016	envelope glycoprot
6	2836.5	81.6	847	2 S13289	env protein - huma
7	2816.5	81.1	852	1 VCLJBR	env polyprotein -
8	2815.5	81.0	855	1 VCLJA2	env polyprotein pr
9	2809.5	80.9	854	2 S13288	env protein - huma
10	2808	80.8	729	1 VCLJRX	env polyprotein pr
11	2808	80.8	861	1 VCLJXB	env polyprotein pr
12	2806.5	80.8	856	1 VCLJH3	env polyprotein pr
13	2799.5	80.6	856	1 VCLJVL	env polyprotein pr
14	2795	80.5	861	1 VCLJLV	env polyprotein pr
15	2782	80.1	851	2 S13985	env polyprotein -
16	2765.5	79.6	861	1 VCLJSC	env polyprotein pr
17	2746	79.0	859	1 VCLJMN	env polyprotein pr
18	2623.5	75.5	853	2 S54384	envelope polyprote
19	2616.5	75.3	855	1 VCLJZR	env polyprotein pr
20	2566	73.9	846	1 VCLJND	env polyprotein pr
21	2550	73.4	856	1 A44963	env polyprotein pr
22	2516	72.4	859	2 T01672	envelope polyprote
23	2130.5	61.3	854	1 VCLJSI	env polyprotein pr
24	2074	59.7	506	2 A40218	envelop glycoprote
25	1909	55.0	495	2 S31493	env polyprotein -
26	1825	52.5	443	2 C41621	env polyprotein p
27	1802	51.9	445	2 A41621	env polyprotein M
28	1751.5	50.4	877	2 S49197	envelope protein p
29	1746.5	50.3	454	2 B41621	env polyprotein D

30	1701.5	49.0	863	2 A53034	gag polyprotein -
31	1204	34.7	297	2 S60538	envelope polyprote
32	1183.5	34.1	859	1 VCLJST	env polyprotein pr
33	1176	33.9	290	2 S25940	env protein - huma
34	1168.5	33.6	712	1 VCLJ84	env polyprotein pr
35	1164.5	33.5	858	1 VCLJG2	env polyprotein pr
36	1157	33.3	852	1 VCLJGG	env polyprotein -
37	1150.5	33.1	877	2 C46356	env polyprotein pr
38	1140	32.8	859	1 VCLJCT	env polyprotein pr
39	1135.5	32.7	869	2 S53098	envelope polyprote
40	1134	32.6	881	2 S03068	env protein - huma
41	1133.5	32.6	864	1 VCLJG4	env polyprotein -
42	1130	32.5	885	2 S04322	env polyprotein -
43	1129.5	32.5	294	2 S60545	envelope polyprote
44	1127.5	32.5	881	1 VCLJG3	env polyprotein -
45	1127	32.4	301	2 S60548	envelope polyprote

ALIGNMENTS

RESULT 1

VCLJH4
env polyprotein - human immunodeficiency virus type 1 (isolate CDC-451)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C:Accession: C25523
R:Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare, Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986
A:Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human A:Reference number: A94136; MUID:87041461; PMID:3490666
A:Accession: C25523
A:Molecule type: DNA
A:Residues: 1-868 <DBS>
A:Cross-references: UNIPROT:P05879; UNIPARC:UPI0000012A014; GB:M13137; NID:g326460; PIDN:
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote
F:1-521/Product: coat protein gp120 #status predicted <GPI>
F:522-868/Product: coat protein gp41 #status predicted <GP2>
F:89,138,139,142,166,195,198,208,245,252,273,287,300,312,342,349,365,371,395,405,409,459
Query Match 100.0%; Score 3474; DB 1; Length 868;
Best Local Similarity 100.0%; Pred. No. 6.4e-247; Mismatches 0; Indels 0; Gaps 0;
Matches 649; Conservative 0;
Qy 1 ANLWVTYVYGVVWKEATTTLCASDAKAYDTEAHNWWATHACVPTNPQEVVLENVTE 60
Db 33 ANLWVTYVYGVVWKEATTTLCASDAKAYDTEAHNWWATHACVPTNPQEVVLENVTE 92
Qy 61 NFNNKNNVVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTTTELSIIVW 120
Db 93 NFNNKNNVVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTTTELSIIVW 152
Qy 121 EQRKGEMRNCSEFNITTSIRDKVQREYALFKLDVEPIDDKNTNTTKVRLNCTSVI 180
Db 153 EQRKGEMRNCSEFNITTSIRDKVQREYALFKLDVEPIDDKNTNTTKVRLNCTSVI 212
Qy 181 TQACPKVSEFPIPHYCTPTGTFALLKCKDKKFKNGTGTCTNVSTVQCTHGIRPVVSTQLLL 240
Db 213 TQACPKVSEFPIPHYCTPTGTFALLKCKDKKFKNGTGTCTNVSTVQCTHGIRPVVSTQLLL 272
Qy 241 NGSLAEBEVIRSENFNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGEI 300
Db 273 NGSLAEBEVIRSENFNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGEI 332
Qy 301 LGNIROAHCNISRAQWNTLQQIATTLREQFGNKTIAFNQSSGGDPBEIVMHSNCGGEFF 360
Db 333 LGNIROAHCNISRAQWNTLQQIATTLREQFGNKTIAFNQSSGGDPBEIVMHSNCGGEFF 392

Qy 361 YCNSQLFNSAWNVTSGTWSVTRKQDGTGDIITLPCRKIQIINRWQVVGKAMVALPIKG 420
Db 393 YCNSQLFNSAWNVTSGTWSVTRKQDGTGDIITLPCRKIQIINRWQVVGKAMVALPIKG 452
Qy 421 LIRCSSNITGLLLTRDGGGNGQTTEIFRPGGDMRDNRSELKYKYKVKIEPLGVAPTAK 480
Db 453 LIRCSSNITGLLLTRDGGGNGQTTEIFRPGGDMRDNRSELKYKYKVKIEPLGVAPTAK 512
Qy 481 KRRVQREKRAVGMGLGAMFLGFLGAAGSTWGTATSMALTVOARQLLSGIVOOOINLLRAIK 540
Db 513 KRRVQREKRAVGMGLGAMFLGFLGAAGSTWGTATSMALTVOARQLLSGIVOOOINLLRAIK 572
Qy 541 AQHLLQLTWGIKQLOARILAVERYLKQDQLGFWGCSGKLICTTAVPNWASNSKNTLD 600
Db 573 AQHLLQLTWGIKQLOARILAVERYLKQDQLGFWGCSGKLICTTAVPNWASNSKNTLD 632
Qy 601 QIWNMTWMEWDREIDNYTHLYTLIBESQOQEKNOQELLQDKWASL 649
Db 633 QIWNMTWMEWDREIDNYTHLYTLIBESQOQEKNOQELLQDKWASL 681

RESULT 2
H44001
env polyprotein precursor - human immunodeficiency virus type 1 (strain YU-2)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: H44001
R:Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
J. Virol. 66, 6587-6600, 1992
A:Title: Complete nucleotide sequence, genome organization, and biological properties of
A:Reference number: A44001; MUID:93021387; PMID:1404605
A:Accession: H44001
A:Molecule type: DNA
A:Residues: 1-843 <LTY>
A:Cross-references: UNIPROT:P35961; UNIPARC:UPI000012A026; GB:M93258
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:19-35/Region: hydrophobic
F:30-489/Product: coat protein gp120 #status predicted <GP1>
F:490-843/Product: coat protein gp41 #status predicted <GP2>
F:499-515/Region: hydrophobic
F:673-689/Region: hydrophobic
F:738-755/Domain: transmembrane #status predicted <TMN>
F:87,129,135,138,154,158,184,193,230,237,258,272,285,291,297,327,351,381,389,395,400,435

Query Match 82.6%; Score 2869.5; DB 1; Length 843;
Best Local Similarity 83.5%; Pred. No. 1.5e-202;
Matches 541; Conservative 35; Mismatches 47; Indels 25; Gaps 6;

Qy 3 LWTVYGVVPWKEATTLFCASDAKAYDEAHNVWATHACVPTNPQSVLENTENF 62
Db 33 LWTVYGVVPWKEATTLFCASDAKAYDEAHNVWATHACVPTNPQSVLENTENF 92
Qy 63 NMWKNMVQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTNTTSLSIIVVWEQ 122
Db 93 NMWKNMVQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTSSS---WET 146
Qy 123 RGKGMKNCFNITTSIRDKVQREYALFYKLDVEPIDDKNNTNTNTKYLINCVTSITQ 182
Db 147 MEKGEIKNCNFNITTSIRDKVQREYALFYNLVDVVID-----NASYRLISCVTSITQ 199
Qy 183 ACPKVSFEPPIHYCTPTGTFALLKCNCKKFKNGGPGCTNVSTVQCTHGIRPVVSTOLLG 242
Db 200 ACPKVSFEPPIHYCAPAGFAILLKCNCKKFKNGGPGCTNVSTVQCTHGIRPVVSTOLLG 259
Qy 243 SLAEEIVIRSENFNTNAKTIIVQLNVSVBINTCRPNNTKRKRVTLGPGRVWVYTTGILG 302
Db 243 SLAEEIVIRSENFNTNAKTIIVQLNVSVBINTCRPNNTKRKRVTLGPGRVWVYTTGILG 302

Db 260 SLAEEIVIRSENFNTNAKTIIVQLNVSVBINTCRPNNTKRKINIGPRALVTTGIIIG 319
Qy 303 NIRQAHCNISRAOWNTLQOIATTLREQFG-NKTIAPNOSSGDPEIVMHSFNCGGFFY 361
Db 320 DIRQAHCNLSKTOWENTLQOIAIKKEQPGNKTIIIFNPSSGGDPEIVTHSFNCGGFFY 379
Qy 362 CNSTQLFNSAWNVTSGTWSVTRKQDGTGDIITLPCRKIQIINRWQVVGKAMVALPIKGL 421
Db 380 CNSTQLF-----TWNDTRKLNNTGENTILPCRKIQIINRWQVVGKAMVALPIRQG 429
Qy 422 IRCSSNITGLLLTRDGGGNGQTTEIFRPGGDMRDNRSELKYKYKVKIEPLGVAPTAK 481
Db 430 IRCSSNITGLLLTRDGGGNGQTTEIFRPGGDMRDNRSELKYKYKVKIEPLGVAPTAK 489
Qy 482 RRVQREKRAVGMGLGAMFLGFLGAAGSTWGTATSMALTVOARQLLSGIVOOOINLLRAIK 541
Db 490 RRVQREKRAVG-LGALFLGFLGAAGSTWGAASITLTVQARQLLSGIVOOOINLLRAIEA 548
Qy 542 QHLLQLTWGIKQLOARILAVERYLKQDQLGFWGCSGKLICTTAVPNWASNSKNTLDQ 601
Db 549 QHLLQLTWGIKQLOARILAVERYLRDQQLGFWGCSGKLICTTAVPNWASNSKNTLDQ 608
Qy 602 IWNMTWMEWDREIDNYTHLYTLIBESQOQEKNOQELLQDKWASL 649
Db 609 IWNMTWMEWDREIDNYTHLYTLIBESQOQEKNOQELLQDKWASL 656

RESULT 3
VCLJ3W
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
C:Accession: A24774
R:Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, B.E.
Cell 45, 637-648, 1986
A:Title: Identification and characterization of conserved and variable regions in the en
A:Reference number: A24774; MUID:86218077; PMID:2423250
A:Accession: A24774
A:Molecule type: DNA
A:Residues: 1-856 <STA>
A:Cross-references: UNIPROT:P31872; UNIPARC:UPI000012A024; GB:M38432; NID:g19(
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-501/Product: coat protein gp120 #status predicted <GP1>
F:502-847/Product: coat protein gp41 #status predicted <GP2>
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459,

Query Match 82.3%; Score 2858; DB 1; Length 856;
Best Local Similarity 82.8%; Pred. No. 1.1e-201;
Matches 539; Conservative 34; Mismatches 60; Indels 18; Gaps 5;

Qy 3 LWTVYGVVPWKEATTLFCASDAKAYDEAHNVWATHACVPTNPQSVLENTENF 62
Db 33 LWTVYGVVPWKEATTLFCASDAKAYDEAHNVWATHACVPTNPQSVLENTENF 92
Qy 63 NMWKNMVQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTNTTSLSIIVVWEQ 122
Db 93 NMWKNMVQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTSSS-----ITDWN 140
Qy 123 R---GKGMKNCFNITTSIRDKVQREYALFYKLDVEPIDDKNNTNTNTKYLINCVTSV 179
Db 141 KTIIGGKNCNFNITTSIRDKVQREYALFYKLDVVPVPIKSNNDSSYTRYRLHCNTSV 200
Qy 180 ITQACKVSFEPPIHYCTPTGTFALLKCNCKKFKNGGPGCTNVSTVQCTHGIRPVVSTOLL 239
Db 201 ITQACKVSFEPPIHYCAPAGFAILLKCNCKKFKNGGPGCTNVSTVQCTHGIRPVVSTOLL 260
Qy 240 LNSGLAEEVIRSENFNTNAKTIIVQLNVSVBINTCRPNNTKRKRVTLGPGRVWVYTTG 298
Db 240 LNSGLAEEVIRSENFNTNAKTIIVQLNVSVBINTCRPNNTKRKRVTLGPGRVWVYTTG 298

Db 261 LNSGLAEEIVIRSENFDTNAKTIIVHLNBSVEINCTRPNNVRRHHIGPGAFY-TG 319
Qy 299 EILGNIRQAHCHNISRAQWNNTLQOIATTLREOPGNKTIAFNQSSGGDPEIVMHSFNCGE 358
Db 320 EIRGNIRQAHCHNISRAQWNNTLQOIATTLREOPGNKTIIVFNHSSGGDPEIVTHSFNCGE 379
Qy 359 FFYCNSTOLFNSAWNTSNGTWSVTRKQKDTGDIITLPCRILQIINRWQVGVKAMYPALPI 418
Db 380 FFYCNSTOLFNSAWNTSNGTWSVTRKQKDTGDIITLPCRILQIINRWQVGVKAMYPALPI 438
Qy 419 KGLRCSNITGLLLTRDGGGENTTEIFRPGGDMRDNMRSELYKYKVKIEPLGVAPT 478
Db 439 GGQIRCSNITGLLLTRDGGGSSREEIFRPGGDMRDNMRSELYKYKVKIEPLGVAPT 498
Qy 479 KAKRVQREKRAVGMIGAMPLGFLGAAGSTMGATSMALTVOARQLLSGIVQOQNLLRA 538
Db 499 KAKRVQREKRAVGAICAMPLGFLGAAGSTMGASLTTLTVOARQLLSGIVQOQNLLRA 558
Qy 539 IKAQHLLQLTVMGIGKQIARILAVERYLKDQQLGFWGSGKLICTTAVPWNASWSNKT 598
Db 559 IEAQHLLQLTVMGIGKQIARILAVERYLKDQQLGFWGSGKLICTTAVPWNASWSNKT 618
Qy 599 LDQIWNNTMWEDEIDNYTHLYTLIEESQKQKQELQDLKQWASL 649
Db 619 MDQIWNNTMWEDEIDNYTHLYTLIEESQKQKQELQDLKQWASL 669

RESULT 4
T09448
envelope glycoprotein - human immunodeficiency virus type 1 (strain JRFL)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,
submitted to the EMBL Data Library, July 1996
A:Reference number: Z16673
A:Accession: T09448
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-847 <PAN>
A:Cross-references: UNIPROT:Q75760; UNIPARC:UPI000010C516; EMBL:U63632; NID:G1465777; PI
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein

Query Match 82.0%; Score 2849.5; DB 2; Length 847;
Best Local Similarity 82.8%; Pred. No. 4.4e-201;
Matches 536; Conservative 40; Mismatches 52; Indels 19; Gaps 4;

Qy 3 LWTVYGVVPVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 62
Db 33 LWTVYGVVPVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 92
Qy 63 NMWKNWVEQMHEDIISLWDSQSLKPCVKLTPLCVTLNCTDLNNTNTTSLSIIVVWEQ 122
Db 93 NMWKNWVEQMHEDIISLWDSQSLKPCVKLTPLCVTLNCTDLNNTNTTSLSIIVVWEQ 146
Qy 123 RKGEMRNCSEFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCVTS 182
Db 147 -ERGEIKNCSEFNITTSIRDEYQKAYLFYKLDVVPIDN-----NNTSYRLISCDISVITQ 200
Qy 183 ACPIKVSFEPIPIHYCTPTGFALLKCNCKKFGNGTGPCTNVSTVQCTHGRIPVSTQLLNG 242
Db 201 ACPIKVSFEPIPIHYCAPAGFALLKCNCKTFNGKPCKNVSTVQCTHGRIPVSTQLLNG 260
Qy 243 SLAEEVIRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGILG 302
Db 261 SLAEEVIRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGILG 320
Qy 303 NIRAHCNISRQAWNNTLQOIATTLREOPGNKTIAFNQSSGGDPEIVMHSFNCGEFYC 362
Db 321 DIRQAHCHNISRAQWNNTLQOIATTLREOPGNKTIIVFNHSSGGDPEIVMHSFNCGEFYC 380

Qy 363 NSTOLFNSAWNTSNGTWSVTRKQKDTGDIITLPCRILQIINRWQVGVKAMYPALPIKGLI 422
Db 381 NSTOLFNSAWNTSNGTWSVTRKQKDTGDIITLPCRILQIINRWQVGVKAMYPALPIKGLI 434
Qy 423 RCGSNITGLLLTRDGGGENTTEIFRPGGDMRDNMRSELYKYKVKIEPLGVAPTAKR 482
Db 435 RCGSNITGLLLTRDGGGENTTEIFRPGGDMRDNMRSELYKYKVKIEPLGVAPTAKR 494
Qy 483 RVVQREKRAVGMIGAMPLGFLGAAGSTMGATSMALTVOARQLLSGIVQOQNLLRAKQ 542
Db 495 RVVQREKRAVG-IGAVFLGFLGAAGSTMGASLTTLTVOARQLLSGIVQOQNLLRAEQ 553
Qy 543 QHLLQLTVMGIGKQIARILAVERYLKDQQLGFWGSGKLICTTAVPWNASWSNKTLDQI 602
Db 554 QHLLQLTVMGIGKQIARILAVERYLKDQQLGFWGSGKLICTTAVPWNASWSNKTLDQI 613
Qy 603 WNNMTMWEDEIDNYTHLYTLIEESQKQKQELQDLKQWASL 649
Db 614 WNNMTMWEDEIDNYTHLYTLIEESQKQKQELQDLKQWASL 660

RESULT 5
T12016
envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T12016
R:McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.
AIDS Res. Hum. Retroviruses 14, 329-337, 1998
A:Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in S
A:Reference number: Z17379; MUID:98178716; PMID:9519894
A:Accession: T12016
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-852 <MCC>
A:Cross-references: UNIPROT:O41883; UNIPARC:UPI000010B1F2; EMBL:U90934; NID:G2351783; PI
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein

Query Match 81.7%; Score 2837; DB 2; Length 852;
Best Local Similarity 83.1%; Pred. No. 3.7e-200;
Matches 541; Conservative 35; Mismatches 53; Indels 22; Gaps 8;

Qy 3 LWTVYGVVPVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 62
Db 33 LWTVYGVVPVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 92
Qy 63 NMWKNWVEQMHEDIISLWDSQSLKPCVKLTPLCVTLNCTDLNNTNTTSLSIIVVWEQ 122
Db 93 NMWKNWVEQMHEDIISLWDSQSLKPCVKLTPLCVTLNCTDY-LRNDTNTT-----SN 143
Qy 123 RG---KGEIMRNCSEFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCVTS 178
Db 144 NGGMEGEIKNCSEFNITTSIRGNKQKAYLFYKLDVVPIDN---NTT--TSYRLINCVTS 198
Qy 179 VITQACPKVSFEPIPIHYCTPTGFALLKCNCKKFGNGTGPCTNVSTVQCTHGRIPVSTQL 238
Db 199 VITQACPKVSFEPIPIHYCTPAGFALLKCKKFGNGTGPCTNVSTVQCTHGRIPVSTQL 258
Qy 239 LLNGSLAEEVIRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTG 298
Db 259 LLNGSLAEEVIRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTG 318
Qy 299 EILGNIRQAHCHNISRAQWNNTLQOIATTLREOPGNKTIAFNQSSGGDPEIVMHSFNCGE 358
Db 319 AIIIGDIRQAHCHNISRAQWNNTLQOIATTLREOPGNKTIAFNQSSGGDPEIVMHSFNCGE 378
Qy 359 FFYCNSTOLFNSAWNTSNGTWSVTRKQKDTGDIITLPCRILQIINRWQVGVKAMYPALPI 418
Db 379 FFYCNSTOLFNSAWNTSNGTWSVTRKQKDTGDIITLPCRILQIINRWQVGVKAMYPALPI 435
Qy 419 KGLRCSNITGLLLTRDGGGENTTEIFRPGGDMRDNMRSELYKYKVKIEPLGVAPT 478

Db 436 RQIRCSSNITGILLTRDGGTNNSTNETFRPGGDMRDNRSSELYKYKVVKIEPLGVAPT 495
Qy 479 KAKRVVQREKRAVGMGLGMPFLGAGAGSTMGATSMALTVOARQLLSGIVQOQNLLRA 538
Db 496 KAKRVVQREKRAVG-IGAVFLGFLGAGSTMGAATVLTVOARQLLSGIVQOQNLLRA 554
Qy 539 IKAQHLLQLTVMGIKOLQARILAVERYLKQDQLLGFPGCGSKLICITTAVPWNASWNSKT 598
Db 555 IEAQHLLQLTVMGIKOLQARILAVERYLDRDQLLGLGWSGSKLICITTTVPWNASWNSKS 614
Qy 599 LDQIWNNTWMEWDREIDNTHLYTILIESQKQKNOQELQLDKWASL 649
Db 615 LDKIWNNTWMEWDREIDNTHLYTILIESQKQKNOQKQELLEDKWSL 665

RESULT 6
S13289
env protein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S13289
R;O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.
Nature 348, 69-73, 1990
A;Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A;Reference number: S13288; MUID:91043044; PMID:2172833
A;Accession: S13289
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-847 <OR>
A;Cross-references: UNIPROT:Q75760; UNIPARC:UPI000017861B
C;Superfamily: type E retrovirus env polyprotein

Query Match 81.6%; Score 2836.5; DB 2; Length 847;
Best Local Similarity 82.5%; Pred. No. 4e-200;
Matches 534; Conservative 39; Mismatches 55; Indels 19; Gaps 4;

Qy 3 LWTVYGVVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 62
Db 33 LWTVYGVVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 92
Qy 63 NMKNVQEMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTTNTSIIIVWEQ 122
Db 93 NMKNVQEMHEDIISLWQSLKPCVKLTPLCVTLNCKDVNATNTINDSEGTM----- 146
Qy 123 RGKEMRCSFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTKYRLINCNTSVITQ 182
Db 147 -ERGEIKNCFSNITTSIRDEVOKEYALFYKLDVVPIDN-----NNTSYRLISCDTSVITQ 200
Qy 183 ACPKVSPEPIPIHYCTPTGFALLKCNCKKFGTGPCTNVSTVQCTHGRVPVSTQLLNG 242
Db 201 ACPKISPEPIPIHYCAPAGFALLKCNCKTNGKGPCKNVSTVQCTHGRVPVSTQLLNG 260
Qy 243 SLAEVEVIRSENFNTNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPRVWVTTGELG 302
Db 261 SLAEVEVIRSENFNTNAKTIIVQLKESVEINCTRPNNHTRKSIHIGPGRAFVTTGELG 320
Qy 303 NIQAHCNISRQAHNTLQOIATTLREQFNKTIAPNQSOGGDPPIVMSHFNCGGFFYC 362
Db 321 DIRQAHCNISRQAHNTLQOIVIKLREQFNKTIIVFNHSSGGDPPIVMSHFNCGGFFYC 380
Qy 363 NSTOLENSANVTNSGTWSTVRKQKDTGDIITLPCRILQIINRWQVVKAMYPALPKGLI 422
Db 381 NSTQLNNTNNNTGTS-----NNTGNTITLPCRILQIINRWQVVKAMYPALPKGLI 434
Qy 423 RCSSNITGLLTRDGGGENOTTEIFRPGGDMRDNRSSELYKYKVVKIEPLGVAPTAKR 482
Db 435 RCSSNITGLLTRDGGGENOTTEIFRPGGDMRDNRSSELYKYKVVKIEPLGVAPTAKR 494
Qy 483 RVVQREKRAVGMGLGMPFLGAGAGSTMGATSMALTVOARQLLSGIVQOQNLLRAIKQ 542
Db 495 RVVQREKRAVG-IGAVFLGFLGAGSTMGAASMTLTVOARQLLSGIVQOQNLLRAIEAQ 553

Qy 543 QHLLQLTVMGIKOLQARILAVERYLKQDQLLGFPGCGSKLICITTAVPWNASWNSKTLDQI 602
Db 554 QRLQLTVMGIKOLQARILAVERYLGDQQLLGLGWSGSKLICITTAVPWNASWNSKSLDRI 613
Qy 603 WNNMTWMEWDREIDNTHLYTILIESQKQKNOQELQLDKWASL 649
Db 614 WNNMTWMEWDREIDNTHLYTILIESQKQKNOQKQELLEDKWSL 660

RESULT 7
VCLJBR
env polyprotein - human immunodeficiency virus type 1 (isolate BR)
N;Alternate names: coat polyprotein
N;Contains: coat protein gp120; coat protein gp41
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C;Accession: A31667
R;Anand, R.; Thayer, R.; Srinivasan, A.; Nayyar, S.; Gardner, M.; Luciw, P.; Dandekar, S.
Virology 168, 79-89, 1989
A;Title: Biological and molecular characterization of human immunodeficiency virus (HIV-1)
A;Reference number: A94389; MUID:89085613; PMID:2789516
A;Accession: A31667
A;Molecule type: DNA
A;Residues: 1-852 <ANA>
A;Cross-references: UNIPROT:P12488; UNIPARC:UPI0000174A36
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: capsid protein; coat protein; polyprotein; transmembrane protein
F;1-516/Product: coat protein gp120 #status predicted <CP1>
F;517-852/Product: coat protein gp41 #status predicted <CP2>

Query Match 81.1%; Score 2816.5; DB 1; Length 852;
Best Local Similarity 80.8%; Pred. No. 1.2e-198;
Matches 528; Conservative 53; Mismatches 43; Indels 31; Gaps 7;

Qy 3 LWTVYGVVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 62
Db 34 LWTVYGVVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 93
Qy 63 NMKNVQEMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTTNTSIIIVWEQ 122
Db 94 NMKNVQEMHEDIISLWQSLKPCVKLTPLCVTLNCHDFNATNATNS----- 143
Qy 123 RGK-----GEMRCSFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTKYRLINCNTS 178
Db 144 -GOMEGEMKCSFNITTSIRDKMQKEYALFYKLDVDPIDNDK---TNTRYRLISCNTS 199
Qy 179 VITQACPVSFPIPIHYCTPTGFALLKCNCKKFGTGPCTNVSTVQCTHGRVPVSTQL 238
Db 200 VITQACPVTFFPIPIHYCAPAGFALLKCNCKKFGTGPCTNVSTVQCTHGRVPVSTQL 259
Qy 239 LINGSIAEEVIRSENFNTNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPRVWVTTG 298
Db 260 LINGSIAEEVIRSENFNTNNKTIIVQLNESVEINCTRPNNHTRKRIITWGPVVTG 319
Qy 299 EILGNIRQAHCNISRQAHNTLQOIATTLREQFNKTIAPNQSOGGDPPIVMSHFNCGGE 358
Db 320 QIIGDIRRAHCNLSRSKVENTLKQIVTKLRVQFNKTIIVFNRSOGGDPPIVMSHFNCGGE 379
Qy 359 FFYCSNQLPNSAW--NVTSSGTWSTVRKQKDTGDIITLPCRILQIINRWQVVKAMYPAL 416
Db 380 PFCNTQLPNSWYNTNTGNT-----EGNSPITLPCRILQIINRWQVVKAMYPAL 431
Qy 417 PIKGLIRCSNITGLLTRDGGGENOT--TEIFRPGGDMRDNRSSELYKYKVVKIEPLG 474
Db 432 PIRGQIKCSSNITGLLTRDGGNNNETTDTTEIFRPGGDMRDNRSSELYKYKVVKIEPLG 491
Qy 475 VAPTAKRVVQREKRAVGMGLGMPFLGAGAGSTMGATSMALTVOARQLLSGIVQOQN 534
Db 492 VAPTAKRVVQREKRAVG-LGALFLGFLGAGSTMGAASLTLTVOARQLLSGIVQOQN 550
Qy 535 LLRAIKAQHLLQLTVMGIKOLQARILAVERYLKQDQLLGFPGCGSKLICITTAVPWNASW 594

551 LIMAIEAQOQHLELTVVNGIKQLQARVLAVERYLKQDQLLIGWCSGKLICTTAVPWNASW 610

Qy 595 SNKTKLDQIWNNTWMEWDREIDNTYTHLYTILIBESQOQEKNOQELLQLDKWASL 649

Db 611 SNKSLSDIWDNMTWWEWEREIDNTYTHLYSLIEDSQIQEKNKELLELDKWASL 665

RESULT 8

VCLJAZ2

env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)

N:Alternate names: coat polyprotein

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004

C:Accession: A03976

R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Sch

Science 227, 484-492, 1985

A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).

A:Reference number: A04003; MUID:85090453; PMID:2578227

A:Accession: A03976

A:Molecule type: DNA

A:Residues: 1-855 <SAS>

A:Cross-references: UNIPROT:P03378; UNIPARC:UPI000012A00F; GB:K02007; NID:g328658; PIDN:

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypro

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-509/Product: exterior membrane glycoprotein #status predicted <EXT>

F:510-855/Product: transmembrane glycoprotein #status predicted <TM>

F:87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445,458

F:610,624,636,815/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 81.0%; Score 2815.5; DB 1; Length 855;

Best Local Similarity 81.2%; Pred. No. 1.4e-198;

Matches 528; Conservative 47; Mismatches 58; Indels 17; Gaps 6;

Qy 3 LWTVVYGVVPWKGAETTLTFCASDAKAYDTEAHNVWATHACVPTNPQPQVLENTENF 62

Db 33 LWTVVYGVVPWKGAETTLTFCASDARAYDEVHNVWATHACVPTDNPQVLENTENF 92

Qy 63 NMWKNMVVEQMHEDIISLWQSLKPCVKLTPCLVTLNCTDLNTNTNTTTSIIIVVEQ 122

Db 93 NMWKNMVVEQMHEDIISLWQSLKPCVKLTPCLVTLNCTDLGKATNTSSN-----WKE 146

Qy 123 RGKGMENCSFNITTSIRDQVREYALFYKLDVEPIDDNKNNTNTKYRLINCNTSVITQ 182

Db 147 EIKGEIKNCSFNITTSIRDKIQENALFRNLDVVPIDNASTNTTYNTYRLIHCNRSVITQ 206

Qy 183 ACPKVSPEPIPIHYCTTGALLKCNDDKKNFGPGCTNVTVOCTTGIRVPVSTOLLNG 242

Db 207 ACPKVSPEPIPIHYCTTAGFALLKCNKNTFNGKPGCTNVTVOCTTGIRPVSSTOLLNG 266

Qy 243 SLAEEVVIRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPGRWVTTTGEILG 302

Db 267 SLAEEVVIRSENFNTNAKTIIVQLNESVAINCTRPNNHTRKSIYIGPGRAFHTTGRIG 326

Qy 303 NIROAHNCISRAQWNNTLQOIATTLREQFG-NKTIAFNQSGGDPDEIVMHSFNCGEFFY 361*

Db 327 DIRAHNCISRAQWNNTLEQIVKKLREQFGNKNKTIVFNQSGGDPDEIVMHSFNCGEFFY 386

Qy 362 CNSTOLFNSAENVVT-SNGTWSVTRKQDGTGDIITLPCRIKOILINRQVVCAMVALPIKG 420

Db 387 CNTTQLFNNTWRLNHTEGT-----KGNDT---IILPCRIKOILINMVEGKAMYPPIGG 438

Qy 421 LIRCSNITGLLLTRDGG-GENOTTEIFRPGGDMRDNRSELYKVKVVKIEPLGVAPTK 479

Db 439 QISCSNITGLLLTRDGGTVNDTVEFRPGGDMRDNRSELYKVKVVKIEPLGIAPTK 498

Qy 480 AKRVVOREKRAVGMGLGAMFLGFIIGAAGSTVGATSMALTVOARQLLSGIVQOQNLLRAI 539

Db 499 AKRVVOREKRAVGIIGAMFLGFIIGAAGSTVGAVSLTTLVOARQLLSGIVQOQNLLRAI 558

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Qy 540 KAOQHLLQLTWGIGKIQARILAVERYLKDQQLLFGWCSGKLCITTAVPWNASWNSKTL 599
Db 559 EAOQHLLQLTWGIGKIQARVLAVERYLRDQQLLGIWCSGKLCITTAVPWNASWNSKSL 618
Qy 600 DQIWNNTWMEWDREIDNYTHLYITLIEESONQOEKNOELLQDKWASL 649
Db 619 EDIWNNTWQWEREIDNYTHLYITLIEESONQOEKNOELLQDKWASL 668

RESULT 9
SI3288
env protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Dec-2004
C:Accession: SI3288
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.;
Nature 348, 69-73, 1990
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions
A:Reference number: SI3288; MUD:91043044; PMID:2172833
A:Accession: SI3288
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-854 <OR>
A:Cross-references: UNIPROT:Q85582; UNIPROT:Q72502; UNIPROT:O90178; UNIPROT:Q7

Query Match 80.9%; Score 2809.5; DB 2; Length 854;
Best Local Similarity 82.8%; Pred. No. 3.8e-198;
Matches 539; Conservative 34; Mismatches 57; Indels 21; Gaps 9

Qy 3 LWVTYVYGVVPWEKATTLFCASDAKAYDTBAHNWATHACVPTNPNOEVVLNVTFN 62
Db 34 LWVTYVYGVVPWEKATTLFCASDAKAYDTEVHNWATHACVPTNPNOEVVLNVTFN 93
Qy 63 NMWKNMVQEHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNNTNTNTTSLIIVWBSQ 1222
Db 94 NMWKNMVQEHEDIISLWDQSLKPCVKLTPLCVSLKCTDL--KNDTNTNSSSGRIME- 1500
Qy 123 RGKEMRNCSENIITTSIRDKVQREYALFYKLDVEPIDDNKNTNTNYKRLINCNTSVITQ 1822
Db 151 --KGEIKNCSENIISTIRDKVQKEYAFYKLDIVPID-----NTSYRLISCNTSVITQ 2011
Qy 183 ACPKVSPEPIPHYCTPTGPFALLKCNCKFNGTGCTNVSTVQCTHGIRPVVSTQLLNG 242
Db 202 ACPKVSPEPIPHYCAPAGPAILKCNKTFNGTGCTNVSTVQCTHGIRPVVSTQLLNG 261
Qy 243 SLAEEVYVIRSENFNTNAKTIIVQLNVSEINCTRPNNHTRK--RVTLPGRWVYTTGSI 300
Db 262 SLAEEVYVIRSENFNTNAKTIIVQLNVSVEINCTRPNNTRKSIRIQPGRAFTVIGKI 321
Qy 301 LGNTRQAHCNISRAOWNNTLQIATTLREQFG-NKTIAPNQSOGDPEIVMHSFNCGGEF 359
Db 322 -GNMROAHCNISRAKWNATLKQIASKUREQFGNNKTIIFKSSGGDPEIVTHSFNCGGEF 380
Qy 360 FYCNSTOLFNSAWNVTSNGTWSVTRKQKDTG-DIITLPCRIKQIINRWVGVGKMYALPI 418
Db 381 FYCNSTOLFNSW---FNSTWSTEGSNNTGESDITLPCRIKQFINMWQEVGKMYAPPI 437
Qy 419 KGLRCCSNITGLLLTRDGGNGNQTTEIFRPGGDMRDNRWSELYKYKVKVIEPLGVAPT 478
Db 438 SGQIRCCSNITGLLLTRDGGNNNGSEIFRPGGDMRDNRWSELYKYKVKVIEPLGVAPT 497
Qy 479 KAKERVVQREKRAVGMGLGAMFELFLGAGSTWGATSMALTVOARQLLSGIVQOONLLRA 538
Db 498 KAKERVVQREKRAVG-IGALFLGLGAGSTWGCTSMTLTVQARQLLSDIVQOONLLRA 556
Qy 539 IKAQCHLLQLTWGIGKIQARILAVERYLKDQQLLFGWCSGKLCITTAVPWNASWNSKT 598
Db 557 IEAQCHLLQLTWGIGKIQARILAVERYLKDQQLLGIWCSGKLCITTAVPWNASWNSKS 616
Qy 599 LDQIWNNTWMEWDREIDNYTHLYITLIEESONQOEKNOELLQDKWASL 649
Db 617 LEQIWNNTWMEWDREINNYTHLSLHSLIEESONQOEKNOELLQDKWASL 667

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QY 422 IRCSSNITGLLLTRDGG-----GENQTEIFRPGGDMRDNRSELYKYKVKIEPLGVA 476
D 444 IRCSSNITGLLLTRDGGNTQNNNTSSIEIFRPGGDMRDNRSELYKYKVKIEPLGVA 503
QY 477 PTKARRVQREKAVGMLGAMFLGFLGAAGSTMGATSMALTVOARQLLSGIVQOQNLL 536
D 504 PTKARRVQREKAVG-IGAVFLGFLGAAGSTMGAAAVLTVOARQLLSGIVQOQNLL 562
QY 537 RAIKAQHLLQLTVWGIKQARILAVERYLKDQQLLGFMGCSGKLICTTAVPWNASWSN 596
D 563 RAIDQAQHLLQLTVWGIKQARILAVERYLKDQQLLGFMGCSGKLICTTAVPWNASWSN 622
QY 597 KTLDOIWNMTWMDREIDNYTHLYTLIESQOQEKNOQELLQDKWASL 649
D 623 KSFNEIWNMTWMDREINNYTHLYTLIESQOQEKNOQELLQDKWASL 675

RESULT 12
VCLJH3
env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C;Accession: A03973
R;Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Doranberger, J.A.; Papas, T.S.; Grayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Skaal, F.
Nature 313, 277-284, 1985
A;Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A;Reference number: A93353; MUID:85111123; PMID:2578615
A;Accession: A03973
A;Molecule type: DNA
A;Residues: 1-856 <RAT>
A;Cross-references: UNIPROT:P03375; UNIPARC:UPI000012A010; GB:M15654; GB:K02008; GB:K0200
C;Genetics:
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F;512-856/Product: transmembrane glycoprotein #status predicted <TM>
F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 80.8%; Score 2806.5; DB 1; Length 856;
Best Local Similarity 82.8%; Pred. No. 6.4e-198;
Matches 539; Conservative 35; Mismatches 58; Indels 19; Gaps 9;
QY 3 LWTVYGVVPWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLNVTFN 62
D 34 LWTVYGVVPWKEATTLFCASDAKAYDTEAHNVWATHACVPTDPPQEVVLNVTFN 93
QY 63 NMWKNVQVQMHEDIISLDQSLKPCVKLPLCVLTNCTDLNNTNTNTSLSIIVVWEQ 122
D 94 NMWKNVQVQMHEDIISLDQSLKPCVKLPLCVLSKCTDL--KNDNTNNTSSSGRIME- 150
QY 123 RGKEMRNCSPNITTSIRDKVQREYALFYKLDVEPIDDKNTNNTKYRLINCNTSVITQ 182
D 151 --KGEIKNCSFNISTSRGKQVEYAFYKLDIIPIDN-----DTTSYTLTSCNTSVITQ 203
QY 183 ACPKVSFEPIHYCTPTGFAALLKCNCKENGTCPTNVTSTVQCTHGRPVVSTQLLNG 242
D 204 ACPKVSFEPIHYCAPAGFALLKCNCKNTFNGTCPTNVTSTVQCTHGRPVVSTQLLNG 263
QY 243 SLAEVEVIRSENFTNAKTIIVQLNVSVVEINCTRPNNHTRK--RVTLGPRGVYTTGEI 300
D 264 SLAEVEVIRSANFTDNAKTIIVQLNQSVVEINCTRPNNHTRKSIIRKQGPRAVFTIGKI 323
QY 301 LGNIROAHNISRAQWNNTLQOIATTLRBOFG-NKTIAPNQSSGGDPEIIVHNSFCGGEF 359
D 324 -GNMROAHNISRAKWNNTLKQIDSKLRQOFGNNKTIIPKQSSGGDPEIVTHNSFCGGEF 382
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QY 360 FYCNSTOLNSANNVTSNGTMSVTRKOKDTG-DIITLPCRILKQILNPNVQVVGKAMYALPI 418
D 383 FYCNSTOLFNFSTW---FNSTWSTKSGNNTGSDTITLPCRILKQILNPNVQVVGKAMYAPPI 439
QY 419 KGLIRCSSNITGLLLTRDGGNGQTTEIFRPGGDMRDNRSELYKYKVKIEPLGVAPT 478
D 440 SGOIRCSSNITGLLLTRDGGNSNNESEIFRPGGDMRDNRSELYKYKVKIEPLGVAPT 499
QY 479 KAKRRVVQREKRAVGMGLGAMFLGFLGAAGSTMGATSMALTVOARQLLSGIVQOQNLLRA 538
D 500 KAKRRVVQREKRAVG-IGALFLGFLGAAGSTMGAASTMLTVOARQLLSGIVQOQNLLRA 558
QY 539 IKAQHLLQLTVWGIKQARILAVERYLKDQQLLGFMGCSGKLICTTAVPWNASWSNKT 598
D 559 IEAQHLLQLTVWGIKQARILAVERYLKDQQLLGFMGCSGKLICTTAVPWNASWSNKS 618
QY 599 LDOIWNMTWMDREIDNYTHLYTLIESQOQEKNOQELLQDKWASL 649
D 619 LEQIWNMTWMDREINNYTHLYTLIESQOQEKNOQELLQDKWASL 669

RESULT 13
VCLJVL
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)
N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C;Accession: A03974
R;Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.
Nature 313, 450-458, 1985
A;Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retroviral
A;Reference number: A93355; MUID:85111157; PMID:2982104
A;Accession: A03974
A;Molecule type: DNA
A;Residues: 1-856 <MUE>
A;Cross-references: UNIPROT:P03376; UNIPARC:UPI000012A01F; GB:K02083; NID:9555008; PIDN:
C;Genetics:
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F;512-856/Product: transmembrane glycoprotein #status predicted <TM>
F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 80.6%; Score 2799.5; DB 1; Length 856;
Best Local Similarity 82.5%; Pred. No. 2.1e-197;
Matches 537; Conservative 36; Mismatches 59; Indels 19; Gaps 9;
QY 3 LWTVYGVVPWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPNPQEVVLNVTFN 62
D 34 LWTVYGVVPWKEATTLFCASDAKAYDTEAHNVWATHACVPTDPPQEVVLNVTFN 93
QY 63 NMWKNVQVQMHEDIISLDQSLKPCVKLPLCVLTNCTDLNNTNTNTSLSIIVVWEQ 122
D 94 NMWKNVQVQMHEDIISLDQSLKPCVKLPLCVLSKCTDL--KNDNTNNTSSSGRIME- 150
QY 123 RGKEMRNCSPNITTSIRDKVQREYALFYKLDVEPIDDKNTNNTKYRLINCNTSVITQ 182
D 151 --KGEIKNCSFNISTSRGKQVEYAFYKLDIIPIDN-----DTTSYTLTSCNTSVITQ 203
QY 183 ACPKVSFEPIHYCTPTGFAALLKCNCKENGTCPTNVTSTVQCTHGRPVVSTQLLNG 242
D 204 ACPKVSFEPIHYCAPAGFALLKCNCKNTFNGTCPTNVTSTVQCTHGRPVVSTQLLNG 263
QY 243 SLAEVEVIRSENFTNAKTIIVQLNVSVVEINCTRPNNHTRK--RVTLGPRGVYTTGEI 300
D 264 SLAEVEVIRSANFTDNAKTIIVQLNQSVVEINCTRPNNHTRKSIIRKQGPRAVFTIGKI 323
QY 301 LGNIROAHNISRAQWNNTLQOIATTLRBOFG-NKTIAPNQSSGGDPEIIVHNSFCGGEF 359
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Db 324 -GNNRQAHCHNISRAKWNNTLQIDSKLREQFGNNKTIIPKQSSGGDPPEIVTHSFNCGGF 382
QY 360 FYCNSSTOLFNSAWNVTSGTWSVTRKQKDTG-DIITLPCRILKOLINRWQVVGKAMVALPI 418
Db 383 FYCNSSTOLFNSW---FNSWTSTEGSNNTEGSDTITLPCRILKQFINNMQEVGKAMVAPI 439
QY 419 KGLIRCSNITGLLLTRDGGGENTTEIFRPGGDMRDNRSELYKYKVKIPLGVAPT 478
Db 440 SGQIRCSNITGLLLTRDGGNNNESEIFRPGGDMRDNRSELYKYKVKIPLGVAPT 499
QY 479 KAKRVVQREKRAVGMFLGAMFLGAGTGMATSMALTVOARQLLSGIVQOQNLLRA 538
Db 500 KAKRVVQREKRAVG-IGALFLGFLGAGTGMATSMALTVOARQLLSGIVQOQNLLRA 558
QY 539 IKAQOHLQLTVMGIKOLQARILAVERYLKDQQLLPGWCGSGKLICTTAVPWNASNK 598
Db 559 IEAQOHLQLTVMGIKOLQARILAVERYLKDQQLLPGWCGSGKLICTTAVPWNASNK 618
QY 599 LDQIWNMTWMDREIDNTHLYIYTLIESQOQEKNOQELLDQKWSL 649
Db 619 LEQIWNMTWMDREINNTYSLIHSIIESQOQEKNEQELLELDKWSL 669

RESULT 14
VCLJLV
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N;Alternate names: coat polyprotein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C;Accession: A03975
R;Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A;Title: Nucleotide sequence of the AIDS virus, LAV.
A;Reference number: A90866; MUID:85099333; PMID:2981635
A;Accession: A03975
A;Molecule type: DNA
A;Residues: 1-861 <WAI>
A;Cross-references: UNIPROT:P03377; UNIPARC:UPI000012A013; GB:K02013; NID:G326417; PIDN:
C;Genetics:
A;Gene: env
A;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypro
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-516/Product: exterior membrane glycoprotein #status predicted <EXT>
F;517-861/Product: transmembrane glycoprotein #status predicted <TM>
F;88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411
F;616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) #status predic

Query Match 80.5%; Score 2795; DB 1; Length 861;
Best Local Similarity 82.4%; Pred. No. 4.5e-197;
Matches 539; Conservative 37; Mismatches 58; Indels 20; Gaps 10;

QY 3 LWTVVYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPPOEVVLNVTENF 62
Db 34 LWTVVYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPPOEVVLNVTENF 93

QY 63 NMWKNMVEQMHEDIISLDQSLKPCVKLTPLCVTLNCTDLN---TN---NTNTTETLSIIV 119
Db 94 NMWKNMVEQMHEDIISLDQSLKPCVKLTPLCVSLKCTDLGNATNTNNTSSSGEMW 153

QY 120 WEQRGKGMENCSFNITTSIRDKVQREYALFYKLDVEPIDDNKNTNTNTKYRLINCTSV 179
Db 154 ME---KGEIKNCSFNISIRGKQVEYAFYKLDIIPIDN-----DTSYTLTSCNTSV 205

QY 180 ITQACPKVSPEPIHYCTPTGTFALLKCNCKFKNGTGPCTNVTSTVQCTHGIRPVSTQLL 239
Db 206 ITQACPKVSPEPIHYCAPAGFAILKCNKNTFNGTGPCTNVTSTVQCTHGIRPVSTQLL 265

QY 240 LNSLAEEVVRSENFNTNAKTIIVQLNVSEINCTRPNNHTRK---RVTLGPRVWYTT 297
Db 266 LNSLAEEVVRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKSIQRGPGRAFVTI 325

QY 298 GEILGNIRQAHCHNISRAQWNNTLQIATTLREQFG-NKTIAFNQSSGGDPPEIVHMSFNCG 356
Db 326 GKI-GNNRQAHCHNISRAKWNNTLQIASKLREQFGNNKTIIPKQSSGGDPPEIVTHSFNCG 384
QY 357 GBFFFCNSSTOLFNSAWNVTSGTWSVTRKQKDTG-DIITLPCRILKOLINRWQVVGKAMYA 415
Db 385 GBFFFCNSSTOLFNSW---FNSWTSTEGSNNTEGSDTITLPCRILKQFINNMQEVGKAMYA 441
QY 416 LPIKGLIRCSNITGLLLTRDGGGENTTEIFRPGGDMRDNRSELYKYKVKIPLGV 475
Db 442 PPISSGQIRCSNITGLLLTRDGGNNNGSEIFRPGGDMRDNRSELYKYKVKIPLGV 501
QY 476 APTKARVVQREKRAVGMFLGAMFLGAGTGMATSMALTVOARQLLSGIVQOQNLL 535
Db 502 APTKARVVQREKRAVG-IGALFLGFLGAGTGMATSMALTVOARQLLSGIVQOQNLL 560
QY 536 LRAIKAQOHLQLTVMGIKOLQARILAVERYLKDQQLLPGWCGSGKLICTTAVPWNASWS 595
Db 561 LRAIEAQOHLQLTVMGIKOLQARILAVERYLKDQQLLPGWCGSGKLICTTAVPWNASWS 620
QY 596 NKTLDQIWNMTWMDREIDNTHLYIYTLIESQOQEKNOQELLDQKWSL 649
Db 621 NKSLEQIWNMTWMDREINNTYSLIHSIIESQOQEKNEQELLELDKWSL 674

RESULT 15
S33985
env polyprotein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S33985
R;Carlini, F.
submitted to the EMBL Data Library, November 1991
A;Reference number: S33979
A;Accession: S33985
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-851 <CAR>
A;Cross-references: UNIPROT:Q78243; UNIPARC:UPI00001067CD; EMBL:Z11530; NID:g60192; PIDN:
C;Superfamily: type E retrovirus env polyprotein

Query Match 80.1%; Score 2782; DB 2; Length 851;
Best Local Similarity 82.0%; Pred. No. 4e-196;
Matches 534; Conservative 39; Mismatches 54; Indels 24; Gaps 9;

QY 3 LWTVVYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPPOEVVLNVTENF 62
Db 34 LWTVVYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPPOEVVLNVTENF 93

QY 63 NMWKNMVEQMHEDIISLDQSLKPCVKLTPLCVTLNCTDLNNTNTTETLSIIVVW 122
Db 94 NMWKNMVEQMHEDIISLDQSLKPCVKLTPLCVSLKCTDL---KNDTNTNNTSSSGRIME- 150

QY 123 RGKGMENCSFNITTSIRDKVQREYALFYKLDVEPIDDNKNTNTNTKYRLINCTSVITQ 182
Db 151 ---KGEIKNCSFNISIRGKQVEYAFYKLDIIPIDN-----DTSYTLTSCNTSVITQ 203

QY 183 ACPKVSPEPIHYCTPTGTFALLKCNCKFKNGTGPCTNVTSTVQCTHGIRPVSTQLLNG 242
Db 204 ACPKVSPEPIHYCAPAGFAILKCNKNTFNGTGPCTNVTSTVQCTHGIRPVSTQLLNG 263

QY 243 SLAABEEVVRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKVTL---GPRVWYTTGEI 300
Db 264 SLAABEEVVRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKIRQIRGPGRAFVTIGKI 323

QY 301 LGNIRQAHCHNISRAQWNNTLQIATTLREQFG-NKTIAFNQSSGGDPPEIVHMSFNCG 359
Db 324 -GNNRQAHCHNISRAKWNNTLQIASKLREQFGNNKTIIPKQSSGGDPPEIVTHSFNCG 382

QY 360 FYCNSSTOLFNSAWNVT-SNGTWSVTRKQKDTGDIITLPCRILKOLINRWQVVGKAMVALPI 418
Db 383 FYCNSSTOLFNSWSTWSTKGSNNT-----EGSDTITLPCRILKOLINRWQVVGKAMVAPI 434

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GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on: March 7, 2006, 17:40:55 ; Search time 297.698 Seconds
(without alignments)
1538.097 Million cell updates/sec

Title: US-09-938-406-1_COPY_33_681

Perfect score: 3474

Sequence: 1 ANLWVTYYGVFWKEATTT.....ONQEKNOQLLDKWSL 649

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

*Med. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3474	100.0	868	1 ENV_HVIC4	P05879 human immun
2	2927	84.3	854	2 Q7SVL3_9HIVI	Q7svl3 human immun
3	2908	83.7	854	2 O40222_9HIVI	O40222 human immun
4	2906.5	83.7	853	2 O6UYR2_9HIVI	O6uyr2 human immun
5	2905	83.6	860	2 Q7SVL7_9HIVI	Q7svl7 human immun
6	2900.5	83.5	863	2 Q6UYPO_9HIVI	Q6uypo human immun
7	2899	83.4	852	2 Q7SVL5_9HIVI	Q7svl5 human immun
8	2898.5	83.4	869	2 Q6UYM7_9HIVI	Q6uym7 human immun
9	2896.5	83.4	853	2 Q03811_9HIVI	Q03811 human immun
10	2896.5	83.4	863	2 Q6UYN7_9HIVI	Q6uyn7 human immun
11	2895	83.3	850	2 Q7SVL4_9HIVI	Q7svl4 human immun
12	2893.5	83.3	861	2 Q7SVU4_9HIVI	Q7svu4 human immun
13	2892.5	83.3	867	2 Q6UYPI_9HIVI	Q6uypi human immun
14	2890.5	83.2	851	2 Q52S58_9HIVI	Q52s58 human immun
15	2889.5	83.2	865	2 Q6UYN6_9HIVI	Q6uyn6 human immun
16	2889	83.2	841	2 Q9QKJ1_9HIVI	Q9qkj1 human immun
17	2889	83.2	849	2 Q6UYQ5_9HIVI	Q6uyq5 human immun
18	2889	83.2	862	2 Q7SVU5_9HIVI	Q7svu5 human immun
19	2888.5	83.1	853	2 Q6UYR3_9HIVI	Q6uyr3 human immun
20	2888	83.1	862	2 Q7SVU1_9HIVI	Q7svu1 human immun
21	2887.5	83.1	853	2 Q6UZ37_9HIVI	Q6uz37 human immun
22	2887.5	83.1	861	2 Q7SVI0_9HIVI	Q7svi0 human immun
23	2885.5	83.1	850	2 Q6UYQ1_9HIVI	Q6uyq1 human immun
24	2885.5	83.1	851	2 Q6UZ40_9HIVI	Q6uz40 human immun
25	2885.5	83.1	854	2 Q6TAN8_9HIVI	Q6tan8 human immun
26	2885	83.0	872	2 Q6UYN9_9HIVI	Q6uyn9 human immun
27	2884.5	83.0	851	2 Q6UYR5_9HIVI	Q6uyr5 human immun
28	2884	83.0	852	2 Q6UZ34_9HIVI	Q6uz34 human immun
29	2883.5	83.0	847	1 ENV_HVIS1	P19550 human immun
30	2883.5	83.0	861	2 Q7SVU0_9HIVI	Q7svu0 human immun
31	2883	83.0	862	2 Q7SVU0_9HIVI	Q7svu0 human immun

32	2883	83.0	862	2 Q7SVU3_9HIVI	Q7svu3 human immun
33	2883	83.0	868	2 Q6UYM9_9HIVI	Q6uym9 human immun
34	2881	82.9	866	2 Q6UYN8_9HIVI	Q6uyn8 human immun
35	2880.5	82.9	851	2 Q6UYR7_9HIVI	Q6uyr7 human immun
36	2879.5	82.9	849	2 Q6UYP9_9HIVI	Q6uyp9 human immun
37	2879.5	82.9	861	2 Q7SVJ8_9HIVI	Q7svj8 human immun
38	2879.5	82.9	861	2 Q7SVU6_9HIVI	Q7svu6 human immun
39	2879.5	82.9	861	2 Q7SVU8_9HIVI	Q7svu8 human immun
40	2878.5	82.9	854	2 Q6TAN5_9HIVI	Q6tan5 human immun
41	2877.5	82.8	847	2 Q6BC04_9HIVI	Q6bc04 human immun
42	2876.5	82.8	854	2 Q6TAN7_9HIVI	Q6tan7 human immun
43	2876	82.8	864	2 Q6UYN4_9HIVI	Q6uyn4 human immun
44	2875	82.8	854	2 Q6UZ36_9HIVI	Q6uz36 human immun
45	2874	82.7	850	2 Q6UYQ8_9HIVI	Q6uyq8 human immun

ALIGNMENTS

RESULT 1

ID	ENV_HVIC4	STANDARD	PRT	868 AA
AC	P05879			
DT	01-NOV-1988 (Rel. 09, Created)			
DT	01-NOV-1988 (Rel. 09, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Envelope glycoprotein gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
DE	Name=ENV;			
GN	Human immunodeficiency virus type 1 (isolate CDC-451) (HIV-1).			
OS	Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;			
OC	Lentivirus; Primate lentivirus group.			
OC	NCBI_TaxID=11687;			
OX	[1]			
RN	NUCLEOTIDE SEQUENCE.			
RP	MEDLINE=87041461; PubMed=3490666;			
RX	Desai S.M., Kalyanaram V.S., Rodriguez V., Veronese F., Rahman R., Lusso P.,			
RA	Andersen P.R., Devare S.G.;			
RA	"Molecular cloning and primary nucleotide sequence analysis of a			
RT	distinct human immunodeficiency virus isolate reveal significant			
RT	divergence in its genomic sequences";			
RL	Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384 (1986).			
RN	[2]			
RP	PROTEIN SEQUENCE OF 34-43.			
RX	MEDLINE=90253924; PubMed=2187500;			
RA	Kalyanaram V.S., Rodriguez V., Veronese F., Rahman R., Lusso P.,			
RA	Devico A.L., Copeland T., Oroszian S., Gallo R.C., Sarngadharan M.G.;			
RT	"Characterization of the secreted, native gp120 and gp160 of the human			
RL	immunodeficiency virus type 1.";			
RL	AIDS Res. Hum. Retroviruses 6:371-380 (1990).			

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CC	EMBL; M13137; AAA44311.1; -; Genomic_RNA.
DR	PIR; C25523; VCLJH4.
DR	HSSP; P19549; INEQ.
DR	SMR; P05879; 84-128, 87-212, 206-503, 552-638.
DR	HIV; M13137; ENV\$CDC45.
DR	InterPro; IPR000328; Env GP41.
DR	InterPro; IPR000777; GP120.
DR	Pfam; PF00516; GP120; 1.
DR	Pfam; PF00517; GP41; 1.
KW	AIDS; Capsid protein; Direct protein sequencing; Glycoprotein;
KW	Polyprotein; Signal; Structural protein; Transmembrane.
FT	SIGNAL 1 33
FT	CHAIN 34 522 Exterior membrane glycoprotein.
FT	CHAIN 523 868 Transmembrane glycoprotein.
FT	CARBOHYD 89 89 N-linked (GlcNAc...) (potential).
FT	CARBOHYD 131 131 N-linked (GlcNAc...) (potential).

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FT CARBOHYD 628 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 637 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 649 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 828 N-linked (GlcNAc...) (Potential)
FT DISULFID 55 By similarity.
FT DISULFID 120 By similarity.
FT DISULFID 127 By similarity.
FT DISULFID 132 By similarity.
FT DISULFID 229 By similarity.
FT DISULFID 239 By similarity.
FT DISULFID 307 By similarity.
FT DISULFID 387 By similarity.
FT DISULFID 394 By similarity.
SQ SEQUENCE 868 AA; 11527FC5246F0C8 CRC64;

Query Match 100.0%; Score 3474; DB 1; Length 868;
Best Local Similarity 100.0%; Pred. No. 1e-266;
Matches 649; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLWTVYGVVPVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTE 60
DB 33 ANLWTVYGVVPVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTE 92
QY 61 NFNMKNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNNTNTTNTTSLIIVVW 120
DB 93 NFNMKNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNNTNTTNTTSLIIVVW 152
QY 121 EQRGKEMRNCSEFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCNTSVI 180
DB 153 EQRGKEMRNCSEFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCNTSVI 212
QY 181 TQACPVSFEPIPIHYCTPTGFPALLKCNCKKNGTGPCTNVSTVQCTHGIRPVVSTQILL 240
DB 213 TQACPVSFEPIPIHYCTPTGFPALLKCNCKKNGTGPCTNVSTVQCTHGIRPVVSTQILL 272
QY 241 NGSIAEEVVIRSENFNTNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVWYTTGEI 300
DB 273 NGSIAEEVVIRSENFNTNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVWYTTGEI 332
QY 301 LGNIROAHCNISRAQWNNTLQIATTLREQFGNKTIAFNQSGGDPDEIVMHSFNCGEFF 360
DB 333 LGNIROAHCNISRAQWNNTLQIATTLREQFGNKTIAFNQSGGDPDEIVMHSFNCGEFF 392
QY 361 YCNSTOLFNSAWNVTSGTWSVTRKQDGTDIITLPCRKQIINRQVGVKAMALPIKG 420
DB 393 YCNSTOLFNSAWNVTSGTWSVTRKQDGTDIITLPCRKQIINRQVGVKAMALPIKG 452
QY 421 LIRCSSNITGLLLTRDGGGENQTTEIFRPGGGDMRNRSELYKYKVKIEPLGVAPTAKA 480
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DB 453 LIRCSSNITGLLLTRDGGGENQTTEIFRPGGGDMRNRSELYKYKVKIEPLGVAPTAKA 512
QY 481 KRVRVQREKRAVGMGLGAMFLGFLGAAGSTMGATSMALTVOAROLLISGIVQQNNLLRAIK 540
DB 513 KRVRVQREKRAVGMGLGAMFLGFLGAAGSTMGATSMALTVOAROLLISGIVQQNNLLRAIK 572
QY 541 AQOHLQLTVMGTGKLOQARILAVERYLKDOQLLGFPGWCSGKLICTTAVPWNASWSNKTLD 600
DB 573 AQOHLQLTVMGTGKLOQARILAVERYLKDOQLLGFPGWCSGKLICTTAVPWNASWSNKTLD 632
QY 601 QIWNNTMTWMDREIDNYTHLIYTLIESQNOQEKNOQELLQDKWASL 649
DB 633 QIWNNTMTWMDREIDNYTHLIYTLIESQNOQEKNOQELLQDKWASL 681

RESULT 2
Q7SVL3_9HIV1
ID Q7SVL3_9HIV1 PRELIMINARY; PRT; 854 AA.
AC Q7SVL3_
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22628496; PubMed=12743293;
RX DOI=10.1128/JVI.77.11.6359-6366.2003;
RA Robbins K.E., Lemey P., Pybus O.G., Jaffe H.W., Youngpairoj A.S.,
RA Brown T.M., Salemi M., Vandamme A.M., Kalish M.L.;
RT "U.S. Human immunodeficiency virus type 1 epidemic: date of origin,
RT population history, and characterization of early strains.";
RL J. Virol. 77:6359-6366(2003).
DR EMBL; AY247222; AAP37150.1; -; Genomic_DNA.
DR HSSP; P04578; IDLB.
DR SMR; Q7SVL3; 2-154, 195-489, 538-624.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env.GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 854 AA; 97048 MW; 36379231FF3AF12C CRC64;
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Query Match 84.3%; Score 2927; DB 2; Length 854;
Best Local Similarity 85.5%; Pred. No. 2.8e-223;
Matches 555; Conservative 33; Mismatches 45; Indels 16; Gaps 7;

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QY 3 LNWTVYGVVPVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTE 62
DB 33 LNWTVYGVVPVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTE 92
QY 63 NNMKNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNNTNTTNTTSLIIVVW 122
DB 93 NNMKNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCT--NLRNTNTTSS----WGT 146
QY 123 RKGEMRNCSEFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCNTSVITQ 182
DB 147 MESGEIKNCSEFNITTSIRDKVQREYALFYKLDVVPINDD-NTT--TSYRLINCNTSVITQ 203
QY 183 ACPKVSFEPIPIHYCTPTGFPALLKCNCKKNGTGPCTNVSTVQCTHGIRPVVSTQILL 242
DB 204 ACPKVSFEPIPIHYCTPTGFPALLKCNCKKNGTGPCTNVSTVQCTHGIRPVVSTQILL 263
QY 243 SLAEEVVIRSENFNTNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPGRVWYTTGEILG 302
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DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 853 AA; 96993 MW; 7392BE340C50C4AD CRC64;

Query Match      83.7%; Score 2906.5; DB 2; Length 853;
Best Local Similarity 83.7%; Pred. No. 1.2e-221;
Matches 543; Conservative 46; Mismatches 47; Indels 13; Gaps 7;

Qy 3 LWTVYGVVPWKAEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 62
Db LWTVYGVVPWKAEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 92
Qy 63 NMWKNVVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTTNTTSLIIVW-E 121
Db 93 NMWKNVVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTD-DVRNATSTNS-----SWGK 146
Qy 122 QRGKGMKNCSEFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCNTSVIT 181
Db 147 PMEKEIKNCSEFNITTSIRDKVQREYALFYKLDVVPID--NDSNNTNYRLISCNVSIT 203
Qy 182 QACPKVSEPIPIHYCTPTGFALLKCNCKKFNKGTGCTNVSTVQCTHGIRPVVSTQLLN 241
Db 204 QACPKVSEPIPIHYCAPAGFALLKCNCKKFNKGTGCTNVSTVQCTHGIRPVVSTQLLN 263
Qy 242 GSLAEEVIRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPGRVVYTTGEIL 301
Db 264 GSLAEEVIRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKRSIHIGPGRAFVTTGDI 323
Qy 302 GNIQAHCNISRANWNTLQIATTLREOFGNKTIIAFNOSGGDPEIVMHSFNCGGEFF 360
Db 324 GDIQAHCNISRANWNTLQIATTLREOFGNKTIIAFNOSGGDPEIVMHSFNCGGEFF 383
Qy 361 YCNSTOLFNSAWNVTSGTWSVTRKQKDTGDIITLPCRIKQIINRWQVGVKAMYPALPIK 420
Db 384 YCNSTKLFNSTW-TWNSTWNNTKRSNDTEITLPCRIKQIINRWQVGVKAMYPALPIK 442
Qy 421 LIRCSSNITGLLTRDGGNGQTTEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPTKA 480
Db 443 QIRCSSNITGLLTRDGGNDTSGETEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPTEA 502
Qy 481 KRRVQREKRAVGMGLGAMFLGFLGAGSTWGAATSMALTVOARQLLSGIVQOQNLLRAIK 540
Db 503 KRRVQREKRAVG-IGAMFLGFLGAGSTWGAASVTLTVQARLLLSGIVQOQNLLRAIE 561
Qy 541 AQHLLQLTVWGIKQOLARILAVERYLKDOQLLGFWCGSGKLICTTAVPWNASWNSKTL 600
Db 562 AQHLLQLTVWGIKQOLARILAVERYLKDOQLLGFWCGSGKLICTTAVPWNASWNSKSLN 621
Qy 601 QIWNNTMTWMDREIDNYTHLYITLIESQNQEKNOQELLDKQWASL 649
Db 622 EIWNNMTWMEWEKEIDNYTHLYITLIESQNQEKNOQELLDKQWAL 670

RESULT 5
Q7SVL7_9HIV1
ID Q7SVL7_9HIV1 PRELIMINARY; PRT; 860 AA.
AC Q7SVL7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22628496; PubMed=12743293;
RX [1]
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RX DOI=10.1128/JVI.77.11.6359-6366.2003;
RA Robbins K.E., Lemey P., Pybus O.G., Jaffe H.W., Youngpairoj A.S.,
RA Brown T.M., Salemi M., Vandamme A.M., Kalish M.L.;
RT "U.S. Human immunodeficiency virus type 1 epidemic: date of origin,
RT population history, and characterization of early strains.";
RL J. Virol. 77:6359-6366(2003).
DR EMBL; AY247218; AAP37146.1; -; Genomic_DNA.
DR HSP; P20871; ICE4.
DR SMR; Q7SVL7; 195-496, 541-630.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 860 AA; 97762 MW; A7E185F2BD421590 CRC64;

Query Match      83.6%; Score 2905; DB 2; Length 860;
Best Local Similarity 84.2%; Pred. No. 1.6e-221;
Matches 548; Conservative 41; Mismatches 48; Indels 14; Gaps 7;

Qy 3 LWTVYGVVPWKAEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 62
Db LWTVYGVVPWKAEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 92
Qy 63 NMWKNVVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTTNTTSLIIVWVQ 122
Db 93 NMWKNVVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDL--RNATNTTSS---GGK 146
Qy 123 RKGEMKNCSEFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCNTSVIT 182
Db 147 MEKGEIKNCSEFNITTSIRDKVQREYALFYKLDVVPID--NDSNTSYRLISCNVSIT 203
Qy 183 ACPKVSEPIPIHYCTPTGFALLKCNCKKFNKGTGCTNVSTVQCTHGIRPVVSTQLLNG 242
Db 204 ACPKVSEPIPIHYCTPAGFALLKCNCKKFNKGTGCTNVSTVQCTHGIRPVSTQLLNG 263
Qy 243 SLAEEVIRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPGRVVYTTGEIL 302
Db 264 SLAEEVIRSDNFMDNAKTIIVQLNVSEINCTRPNNHTRKRSIHIGPGRAFVTTGEI 323
Qy 303 NIQAHCNISRANWNTLQIATTLREOFGNKTIIAFNOSGGDPEIVMHSFNCGGEFF 362
Db 324 DIQAHCNISRANWNTLQIATTLREOFGNKTIIAFNOSGGDPEIVMHSFNCGGEFF 383
Qy 363 NSTOLFNSAWN--VTSNGTW-SVTRKQKDTGDIITLPCRIKQIINRWQVGVKAMYPALPIK 419
Db 384 DSTOLFNSAWN--VTSNGTW-SVTRKQKDTGDIITLPCRIKQIINRWQVGVKAMYPALPIK 443
Qy 420 GLIRCSSNITGLLTRDGG-GENQTTEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPT 478
Db 444 QIRCSSNITGLLTRDGGNGQTTEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPT 503
Qy 479 KARRVQREKRAVGMGLGAMFLGFLGAGSTWGAATSMALTVOARQLLSGIVQOQNLLRA 538
Db 504 KARRVQREKRAVG-IGAMFLGFLGAGSTWGAASVTLTVQARLLLSGIVQOQNLLRA 562
Qy 539 IKAQHLLQLTVWGIKQOLARILAVERYLKDOQLLGFWCGSGKLICTTAVPWNASWNSKT 598
Db 563 IEAQHLLQLTVWGIKQOLARILAVERYLKDOQLLGFWCGSGKLICTTAVPWNASWNSKS 622
Qy 599 LQIWNNTMTWMDREIDNYTHLYITLIESQNQEKNOQELLDKQWASL 649
Db 623 LDKIWNNTMTWMDREIDNYTHLYITLIESQNQEKNOQELLDKQWASL 673

RESULT 6
Q6UYPO_9HIV1
ID Q6UYPO_9HIV1 PRELIMINARY; PRT; 863 AA.
AC Q6UYPO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
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DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1490699; DOI=10.1128/JVI.78.6.2790-2807.2004;
RA Kuhlmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L.,
RA Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
RA Korber B.T., Wolinsky S.M., Moore J.P.;
RT "Genetic and phenotypic analyses of human immunodeficiency virus type
RT 1 escape from a small-molecule CCR5 inhibitor."
RL J. Virol. 78:2790-2807(2004)
DR EMBL; AY357551; AAR00905.1; -; Genomic_DNA.
DR HSSP; P04578; 1K33.
DR SMR; Q6UYF0; 93-147, 209-507, 552-641.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON TER
SQ SEQUENCE 863 AA; 98144 MW; 02D82C72985648EC CRC64;

Query Match 83.5%; Score 2900.5; DB 2; Length 863;
Best Local Similarity 83.5%; Pred. No. 3.6e-221;
Matches 545; Conservative 45; Mismatches 50; Indels 13; Gaps 8;

QY 2 NLWTVVYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTEN 61
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 40 NLWTVVYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTEN 99
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 62 FNMWKNVVEQMHEDIISLWQSLKPCVKLPLCVTLNCTDLN--TNNTNTTSLIIVW 120
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 100 FNMWKNVVEQMHEDIISLWQSLKPCVKLPLCVTLNCTDLN--TNNTNTTSLIIVW 154
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 -EQRKGEMRNCNFTTTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCNTSV 179
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 155 GEPMEKEIKNCNFTTTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCNTSV 214
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 180 ITQACPKVSEPIPIHYCTPTGFPALLKCKDKKFGTGPCTNVSTVQCTHGIRPVVSTQLL 239
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 215 ITQACPKVSEPIPIHYCAPAGFALICKDKKFGTGPCTNVSTVQCTHGIRPVVSTQLL 274
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 240 LKNGSLAEVEVIRSENFTNNAKTIIVQLNVSVVEINCTRPNNHTRKRVTLGPRVWYTTGE 299
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 275 LKNGSLAEVEVIRSENFTNNAKTIIVQLNVSVVEINCTRPNNHTRKRVTLGPRVWYTTGE 334
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 300 ILGNIRQAHNCISRAQWNTLQOIATTLREQFG-NKTIAPQSSGGDPEIVMHSFNCGGE 358
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 335 IIGDIRKAHCNISRAQWNTLKHIVKLGKQFGNKTIVFNHSSGGDPEIVMHSFNCGGE 394
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 359 FFYCNSTQLFNSAWNTVSGTW--SVTRKQKDTGDIITLPCRKQIINRWQVVKAMVAL 416
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 395 FFYCNSTQLFNSAWNTVSGTW--SVTRKQKDTGDIITLPCRKQIINRWQVVKAMVAL 453
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 417 PIKGLIRCSNITGLLLTRDGGGNOTTEIFRPGGDMRDNRSSELYKYKVVKEPLGVA 476
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 454 PIKGLIRCSNITGLLLTRD--GGTNTNTETFRPGGDMRDNRSSELYKYKVVKEPLGVA 512
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 477 PTKARRVVOREKRAVGLGAMFGLGAGSTMGATSMALTVOARQLLSGIIVQOQNLL 536
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 513 PTEAKRRVVOREKRAVG-IGAVLLGFLGAGSTWGAASVTLTVQARQLLSGIIVQOQNLL 571
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 537 RAIKAQHLLQLTWGIKQLQARILAVERYLKDQQLGFWCSCGKI.ICTTAVPWNASHN 596
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 572 RAIKAQHLLQLTWGIKQLQARILAVERYLKDQQLGFWCSCGKI.ICTTAVPWNASHN 631
QY 597 KTLDOIWNNTWMEWDREIDNYTHLYTLIBESQOQKQQLQLDQKWL 649
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 632 KSMDEIWNNTWMEWKEIDNYTGLIYNLLEKSNQOQKQQLDQKWL 684
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 7
Q7SVL5_9HIV1 PRELIMINARY; PRT; 852 AA.
AC Q7SVL5;
DT 01-OCT-2003 (TREMblrel. 25, Created)
DT 01-OCT-2003 (TREMblrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22628496; PubMed=12743293;
RA DOI=10.1128/JVI.77.11.5359-5366.2003;
RA Robbins K.E., Lemey P., Pybus O.G., Jaffe H.W., Youngpairoj A.S.,
RA Brown T.M., Salemi M., Vandamme A.M., Kallish M.L.;
RT "U.S. Human immunodeficiency virus type 1 epidemic: date of origin,
RT population history, and characterization of early strains."
RL J. Virol. 77:6359-6366(2003)
DR EMBL; AY247220; AAP37148.1; -; Genomic_DNA.
DR HSSP; P04578; 1DLB.
DR SMR; Q7SVL5; 536-622.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 852 AA; 96680 MW; F8D811028035D998 CRC64;

Query Match 83.4%; Score 2899; DB 2; Length 852;
Best Local Similarity 83.9%; Pred. No. 4.7e-221;
Matches 546; Conservative 36; Mismatches 47; Indels 22; Gaps 6;

QY 3 LWTVVYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 62
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 33 LWTVVYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 92
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 63 NMWKNVVEQMHEDIISLWQSLKPCVKLPLCVTLNCTDLNNTNTTNTTSLIIVW 122
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 93 NMWKNVVEQMHEDIISLWQSLKPCVKLPLCVTLNCTDLN--GNTNTTSS----- 143
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 123 RG----KGEKNCNFTTTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCNTS 178
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 144 -GGMERGEIKNCNFTTTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCNTS 197
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 179 VITQACPKVSEPIPIHYCTPTGFPALLKCKDKKFGTGPCTNVSTVQCTHGIRPVVSTQL 238
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 198 VITQACPKVSEPIPIHYCAPAGFALICKDKKFGTGPCTNVSTVQCTHGIRPVVSTQL 257
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 239 LKNGSLAEVEVIRSENFTNNAKTIIVQLNVSVVEINCTRPNNHTRKRVTLGPRVWYTTG 298
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 258 LKNGSLAEVEVIRSENFTNNAKTIIVQLNVSVVEINCTRPNNHTRKRVTLGPRVWYTTG 317
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 299 EILGNIRQAHNCISRAQWNTLQOIATTLREQFGNKTIVFNHSSGGDPEIVMHSFNCGGE 358
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 318 DIVGDIRQAHNCISRAQWNTLQOIATTLREQFGNKTIVFNHSSGGDPEIVMHSFNCGGE 377
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 359 FFYCNSTQLFNSAWNTVSGTW--SVTRKQKDTGDIITLPCRKQIINRWQVVKAMVALPI 418
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 378 FFYCNSTQLFNSAWNTVSGTW--SVTRKQKDTGDIITLPCRKQIINRWQVVKAMVALPI 435
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY 419 KGLRCSNITGLLLTRDGGGENTTEIFRPGGDMRDNRSELYKYKVKIEPLGVAPT 478
D 436 RGQIRCSNITGLLLTRDGGGENDTEIFRPGGDMRDNRSELYKYKVKIEPLGVAPT 495
QY 479 KAKRVVQREKRAVGMGLGFLGAGSTMGATSMALTVOARQLLSGIVQQNNLLRA 538
D 496 KAKRVVQREKRAVG-IGAVFLGFLGAGSTMGAASTMTLTVOARQLLSGIVQQNNLLRA 554
QY 539 IKAQHLLQLTVMGIKQOLQARILAVERYLKDOQLLGFWCGSGKLICTTAVPWNASWNTK 598
D 555 IEAQHLLQLTVMGIKQOLQARVLAVERYLKDOQLLGFWCGSGKLICTTAVPWNASWNTK 614
QY 599 LDQIWNNTWMEWDREIDNTHTLYTLIESQNOQKNOQELLQLDKWSL 649
D 615 LDNIWNNTWMEWDREINNTSLYTLIESQNOQKNEQELLELDKWSL 665

RESULT 8
Q6UYM7_9HIV1
ID Q6UYM7_9HIV1 PRELIMINARY; PRT; 869 AA.
AC Q6UYM7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14990699; DOI=10.1126/JVI.78.6.2790-2807.2004;
RA Kuhnmann S.E., Pugach P., Kunsman K.J., Taylor J., Stanfield R.L.,
RA Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
RA Korber B.T., Wolinsky S.M., Moore J.P.;
RT "Genetic and phenotypic analyses of human immunodeficiency virus type
RT 1 escape from a small-molecule CCR5 inhibitor.";
RL J. Virol. 78:2790-2807(2004).
DR EMBL; AY357566; AAR00918.1; -; Genomic_DNA.
DR SBL; Q6UYM7; 90-134, 561-647.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON TER 1
SQ SEQUENCE 869 AA; 99123 MW; FE2BE1E50EF1CC9A CRC64;

Query Match 83.4%; Score 2896.5; DB 2; Length 869;
Best Local Similarity 82.5%; Pred. No. 5.3e-221;
Matches 543; Conservative 48; Mismatches 50; Indels 17; Gaps 8;

QY 2 NLWVTYVYGVVWKKEATTTILFCASDAKAYDTEAHNVWATHACVPTNPQEVVLENTEN 61
D 40 NLWVTYVYGVVWKKEATTTILFCASDAKAYDTEAHNVWATHACVPTNPQEVVLENTEN 99
QY 62 FNNWKNMVQEMHEDIISLDQSLKPCVKLTPLCVTLNCTDL--NTNNTNTTSLIIV 118
D 100 FNNWKNMVQEMHEDIISLDQSLKPCVKLTPLCVTLNCTDYVKNATNTNTN----- 154
QY 119 VW-EQRGKGBMRNCSEFNITSDIRKQVREYALFYKLDVEPID--NKNTTN--TKYRL 172
D 155 SWGEPMEKGEIKNCSEFNITSDIRKQVREYALFYKLDVEPIDNDSNNNSNNNTNYRL 214
QY 173 INCNTSVITACPKVSEFPIPIHYCTPTGPAKLCNDKPKFNGPGCTNVSTVQCTHGIRP 232
D 215 INCNTSVITACPKVSEFPIPIHYCAPAGPAKLCNDKPKFNGPGCTNVSTVQCTHGIRP 274

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QY 233 VVSTQLLLSGLAEVEEVIRESNFTNNAKTIIIVQLNVSVBEINCTRPNNHTRKRVTLGPGR 292
D 275 VVSTQLLLSGLAEVEEVIRESNFTNNAKTIIIVQLNVSVBEINCTRPNNHTRKRVTLGPGR 334
QY 293 VYTTGEILGNITROAHNCNISRAQNNNTLQOIATTLREQFGNKTIATFQSSGGDPPEIVMHS 352
D 335 VYTTGEIVGDIRKAHCNISRTQNNNTLKHIVEKLGKQFGNNKTIFNHSSGGDPPEIVMHS 394
QY 353 FNCGGEFFYCNSTQLFNSANWVTSNGTSWTRQKQTDITLPCRIKQIINWQVVGKA 412
D 395 FNCGGEFFYCNSTKLFNSTW--TRNNDTWT--TERSNSTEHTLPCRIKQIINWQVVGKA 452
QY 413 MYALPTKGLIRCSNITGLLLTRDGG-GENOTTEIFRPGGDMRDNRSELYKYKVKIE 471
D 453 VIAPPTRGKIRCSNITGLLLTRDGGNNDTRGTEIFRPGGDMRDNRSELYKYKVKIE 512
QY 472 PLGVAPTAKRRVVRQREKRAVGMGLGFLGAGSTMGATSMALTVOARQLLSGIVQQ 531
D 513 PLGIAPTEAKRRVVRQREKRAVGMGLGFLGAGSTMGAASTVALTVOARQLLSGIVQQ 572
QY 532 QNNLIRAIKAOQHLLQLTVMGIKQOLQARILAVERYLKDOQLLGFWCGSGKLICTTAVPWN 591
D 573 QNNLIRAIKAOQHLLQLTVMGIKQOLQARILAVERYLKDOQLLGFWCGSGKLICTTAVPWN 632
QY 592 ASWSNKTLDQIWNNTWMEWDREIDNTHTLYTLIESQNOQKNOQELLQLDKWSL 649
D 633 ASWSNRSIDEIWNNTWMEWEKEIDNTHTLYTLIESQNOQKNEQELLELDKWSL 690

RESULT 9
Q03811_9HIV1
ID Q03811_9HIV1 PRELIMINARY; PRT; 853 AA.
AC Q03811;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Surface envelope glycoprotein.
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91195299; PubMed=2014229;
RA Westervelt P., Gendelman H.E., Ratner L.;
RT "Identification of a determinant within the human immunodeficiency
RT virus 1 surface envelope glycoprotein critical for productive
RT infection of primary monocytes.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:3097-3101(1991).
DR EMBL; M50472; AAA45065.1; -; Genomic_RNA.
DR HSSP; P20871; ICE4.
DR SNR; Q03811; 143-488, 537-623.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 853 AA; 96998 MW; AD2AF21E2B06AD78 CRC64;

Query Match 83.4%; Score 2896.5; DB 2; Length 853;
Best Local Similarity 83.6%; Pred. No. 7.4e-221;
Matches 544; Conservative 40; Mismatches 48; Indels 19; Gaps 6;

QY 2 NLWVTYVYGVVWKKEATTTILFCASDAKAYDTEAHNVWATHACVPTNPQEVVLENTEN 61
D 32 NLWVTYVYGVVWKKEATTTILFCASDAKAYDTEAHNVWATHACVPTNPQEVVLENTEN 91
QY 62 FNNWKNMVQEMHEDIISLDQSLKPCVKLTPLCVTLNCTDL--NTNNTNTTSLIIV 120
D 92 FNNWKNMVQEMHEDIISLDQSLKPCVKLTPLCVTLNCTDLRNVTNINNSSE----- 144

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Qy 121 EQRKGEMRNCSENIITTSIRKQVREYALFYKLDVEPIDDNKNTTNTKYLINCNTSVI 180
Db 145 --GMRGEIKNCSENIITTSIRKQVREYALFYKLDVEPIDN-----DNTSVYRLINCNTSTI 197

Qy 181 TQACPVSFEBPIPIHYCTPTGTFALLKNDKFKNGTGPCTNVSTVQCTHGIRPVVSTQALL 240
Db 198 TQACPVSFEBPIPIHYCTPAGFAILKCKDKFKNGTGPCKNVSTVQCTHGIRPVVSTQALL 257

Qy 241 NGS�ABEEVIRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPGRVYTTGEI 300
Db 258 NGS�ABEEVIRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPGRVYTTGEI 317

Qy 301 LGNIRQAHNCISRAQWNTTLOQIATTLREQFG-NKTIAPNOSGSGDPEIVMHSFNCGGEF 359
Db 318 IGDIRQAHNCISRAQWNTTLOQIATTLREQFG-NKTIAPNOSGSGDPEIVMHSFNCGGEF 377

Qy 360 FYCNSQTLFNSAMWNTSGTWSVTRKQKDTG-DIITLPCRIKQIINRWQVVGKAMYPPI 418
Db 378 FYCNSQTLFNSAMWNTSGTWSVTRKQKDTG-DIITLPCRIKQIINRWQVVGKAMYPPI 435

Qy 419 KGLIRCSNITGLLLTRDGGENQTEIFRPGGDMRDNWSELYKYKVVKIEPLGVAPT 478
Db 436 RGQIRCSNITGLLLTRDGGENQTEIFRPGGDMRDNWSELYKYKVVKIEPLGVAPT 495

Qy 479 KAKRVVQREKRAVGMGLMFLGAGSTMGATSMALTVOARQLLSGIVQOQNLLRA 538
Db 496 KAKRVVQREKRAVGMGLMFLGAGSTMGATSMALTVOARQLLSGIVQOQNLLRA 555

Qy 539 IKAQHLLQLTVMGIKQIARILAVERYLKDQQLLGFWCGSGKLCICTTAVPWNASWKNKT 598
Db 556 IEAQHLLQLTVMGIKQIARILAVERYLKDQQLLGFWCGSGKLCICTTAVPWNASWKNKT 615

Qy 599 LDQIWNNTWMEWDREIDNYTHLYTLIEESQOQKQOELLQDKWASL 649
Db 616 LDMIWNTWMEWDREIDNYTHLYTLIEESQOQKQOELLQDKWASL 666

RESULT 10
Q6UYN7_9HIV1
ID Q6UYN7_9HIV1 PRELIMINARY; PRT; 863 AA.
AC Q6UYN7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;
RA Kuhnman S.E., Pugach P., Kunstman K.J., Taylor J., Scanfield R.L.,
RA Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
RA Korber B.T., Wolinsky S.M., Moore J.P.;
RT "Genetic and phenotypic analyses of human immunodeficiency virus type
RT 1 escape from a small-molecule CCR5 inhibitor."
RL J. Virol. 78:2790-2807(2004).
DR EMBL; AY357554; AAR00908.1; -; Genomic_DNA.
DR HSSP; P04578; 1K33.
DR SMR; Q6UYN7; 93-147; 209-507; 555-641.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON TER
SQ SEQUENCE 863 AA; 98318 MW; DE3DF76BF7B54E5C CRC64;

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Query Match 83.4%; Score 2896.5; DB 2; Length 863;
Best Local Similarity 82.9%; Pred. No. 7.6e-221;
Matches 544; Conservative 45; Mismatches 48; Indels 19; Gaps 8;

Qy 2 NLWVTVYGVVWKEATTTILFCASDAKAYDTEAHNVWATHACVPTNPPOBVLNVTEN 61
Db 40 NLWVTVYGVVWKEATTTILFCASDAKAYDTEAHNVWATHACVPTNPPOBVLNVTEN 99

Qy 62 FNMWKNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLN-TNNTNTTTELSIIVW 120
Db 100 FNMWKNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDKNTTNNATSTNS-----SW 154

Qy 121 -EQGKGEMRNCSENIITTSIRKQVREYALFYKLDVEPIDDNKNTTNTKYLINCNTSV 179
Db 155 GEPMEKEIKNCSENIITTSIRKQVREYALFYKLDVEPIDDNKNTTNTKYLINCNTSV 214

Qy 180 ITQACPVSFEBPIPIHYCTPTGTFALLKNDKFKNGTGPCTNVSTVQCTHGIRPVVSTQALL 239
Db 215 ITQACPVSFEBPIPIHYCAPAGFAILKNDKFKNGTGPCTNVSTVQCTHGIRPVVSTQALL 274

Qy 240 LNSLABEEVIRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPGRVYTTGE 299
Db 275 LNSLABEEVIRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPGRVYTTGE 334

Qy 300 ILGNIRQAHNCISRAQWNTTLOQIATTLREQFG-NKTIAPNOSGSGDPEIVMHSFNCGGE 358
Db 335 IIGDIRQAHNCISRAQWNTTLOQIATTLREQFG-NKTIAPNOSGSGDPEIVMHSFNCGGE 394

Qy 359 FFYCNSTOLFNSAMWNTSGTWSVTRKQKDTG-DIITLPCRIKQIINRWQVVGKAM 413
Db 395 FFYCNSTOLFNSAMWNTSGTWSVTRKQKDTG-DIITLPCRIKQIINRWQVVGKAM 449

Qy 414 YALPIKGLIRCSNITGLLLTRDGGENQTEIFRPGGDMRDNWSELYKYKVVKIEPL 473
Db 450 YALPIKGLIRCSNITGLLLTRDGGENDTSRIEIRPGGDMRDNWSELYKYKVVKIEPL 509

Qy 474 GVAPTAKRRVQREKRAVGMGLMFLGAGSTMGATSMALTVOARQLLSGIVQOQN 533
Db 510 GIAPTAKRRVQREKRAVGMGLMFLGAGSTMGATSMALTVOARQLLSGIVQOQN 568

Qy 534 NLRAIKAQOHLQLTVMGIKQIARILAVERYLKDQQLLGFWCGSGKLCICTTAVPWNAS 593
Db 569 NLRAIKAQOHLQLTVMGIKQIARILAVERYLKDQQLLGFWCGSGKLCICTTAVPWNAS 628

Qy 594 WSNKTLDOIWNNTWMEWDREIDNYTHLYTLIEESQOQKQOELLQDKWASL 649
Db 629 WSNKTLDOIWNNTWMEWDREIDNYTHLYTLIEESQOQKQOELLQDKWASL 684

RESULT 11
Q7SVLA_9HIV1
ID Q7SVLA_9HIV1 PRELIMINARY; PRT; 850 AA.
AC Q7SVLA;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22628496; Pubmed=12743293;
RX DOI=10.1128/JVI.77.11.6359-6366.2003;
RA Robbins K.E., Lemey P., Pybus O.G., Jaffe H.W., Youngpairaj A.S.,
RA Brown T.M., Salemi M., Vandamme A.M., Kalish M.L.;
RT "U.S. Human immunodeficiency virus type 1 epidemic: date of origin,
RT population history, and characterization of early strains."
RL J. Virol. 77:6359-6366(2003).
DR EMBL; AY247221; AAP37149.1; -; Genomic_DNA.

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DR HSP; P20871; 1CE4.
DR SMR; Q7SVL4; 195-486, 534-620.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 850 AA; 96583 MW; 62ED5F6AB033D20B CRC64;

Query Match 83.3%; Score 2895; DB 2; Length 850;
Best Local Similarity 84.9%; Pred. No. 9.7e-221;
Matches 552; Conservative 33; Mismatches 43; Indels 22; Gaps 8;

Qy 3 LNWTVYGVVPWKKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTENF 62
Db |||||
Qy 33 LNWTVYGVVPWKKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTENF 92
Db |||||
Qy 63 NMWKNMVQEHEDIISLWQSLKPCVKLPLCVLTNCTDLNTNTNTTSLSIIVVWEQ 122
Db |||||
Qy 93 NMWKNMVQEHEDIISLWQSLKPCVKLPLCVLTNCTDL--RNAITNTSSS---GGT 146
Db |||||
Qy 123 RGKGMNCSFNITTSIRDVKQREYALFYKLDVEPIDDNKNTNTNTKYRLINCNTSVITQ 182
Db |||||
Qy 147 MERGEIKNCSFNITTSIRDVKQREYALFYKLDVPI-DNDNTT--TSYRLISCNTSVITQ 203
Db |||||
Qy 183 ACPKVSEPIPIHYCTPTGFPALLKCNCKKNGTGPCTNVSTVQCTHGIRPVSTQLLNG 242
Db |||||
Qy 204 ACPKVSEPIPIHYCTPTGFPALLKCNCKKNGTGPCTNVSTVQCTHGIRPVSTQLLNG 263
Db |||||
Qy 243 SLAEVVVIRSENFTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWVTTGEILG 302
Db |||||
Qy 264 SLAEVVVIRSDNFDNAKTIIVQLKESVEINCTRPNNHTRKSIHIGFGRAFVTTGSIIG 323
Db |||||
Qy 303 NIQAHCNISRAQWNTLQOIATTLREQFGNKTIATFNQSSGGDPEIVMHSFNCGGFFYC 362
Db |||||
Qy 324 DIRQAHCNLSRAKWDNLKQIVRKLEQFGNKTIIVFNQSSGGDPEIVTHSFNCGGFFYC 383
Db |||||
Qy 363 NSTOLFNSANVT--SNGTWSVTRKQKDTGDI-ITLPCRKQIINRWQVVGKAMYLPIK 419
Db |||||
Qy 384 DSTOLFNSTVNTGSSNT-----EGNITLTPCRKQIINRWQVVGKAMYPPIR 434
Db |||||
Qy 420 GLIRCSSNITGLLTRDGGNGNTEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPTK 479
Db |||||
Qy 435 GQIRCSSNITGLLTRDGGNGNESEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPTK 494
Db |||||
Qy 480 AKRRVQREKRAVGMFLGAMFLGFLGAAGSTMGATSMALTVOARQLLSGIVQQNNLLRAI 539
Db |||||
Qy 495 AKRRVQREKRAVG-IGAVFLGFLGAAGSTMGASMTLTVOARQLLSGIVQQNNLLRAI 553
Db |||||
Qy 540 KAQHLQLTWTGKIQLOARILAVERYLKDQQLLGFPGWCSGKLCITTAVPWNASWNTKL 599
Db |||||
Qy 554 EAQHLQLTWTGKIQLOARILAVERYLKDQQLLGFPGWCSGKLCITTVPNWASWNSKSL 613
Db |||||
Qy 600 DOIWNMTWMEDEIDNYTHLYTLIEESQNOQKQOELLQLDKWSL 649
Db |||||
Qy 614 DKIWNNMTWMEDEIDNYTHLYTLIEESQNOQKQOELLQLDKWSL 663
Db |||||

RESULT 12

Q7SVL4_9HIV1
ID Q7SVL4_9HIV1 PRELIMINARY; PRT; 861 AA.
AC Q7SVL4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.

OX NCB1_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22533916; PubMed=12646921; DOI=10.1038/nature01470;
RA Wei X., Decker J.M., Wang S., Hui H., Kappes J.C., Wu X.,
RA Salazar-Gonzalez J.F., Salazar M.G., Kilby J.M., Saag M.S.,
RA Komarova N.L., Nowak M.A., Hahn B.H., Kwong P.D., Shaw G.M.;
RT "Antibody neutralization and escape by HIV-1.";
RL Nature 422:307-312(2003).
DR ENBL; AY223724; AAP57324.1; -; Genomic_RNA.
DR HSP; P04578; IDLB.
DR SMR; Q7SVL4; 545-631.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 861 AA; 98313 MW; 4E8A3F4278A9E302 CRC64;

Query Match 83.3%; Score 2893.5; DB 2; Length 861;
Best Local Similarity 83.1%; Pred. No. 1.3e-220;
Matches 544; Conservative 42; Mismatches 50; Indels 19; Gaps 7;

Qy 2 LNWTVYGVVPWKKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTEN 61
Db |||||
Qy 32 LNWTVYGVVPWKKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTEN 91
Db |||||
Qy 62 FMWKNMVQEHEDIISLWQSLKPCVKLPLCVLTNCTDLNTNTNTTSLSIIVWE 121
Db |||||
Qy 92 FMWKNMVQEHEDIISLWQSLKPCVKLPLCVLTNCTDL--KNATNTSIK-----E 144
Db |||||
Qy 122 QRGKGMNCSFNITTSIRDVKQREYALFYKLDVEPIDDNKNTNTNTKYRLINCNTSVIT 181
Db |||||
Qy 145 REMRGEIKNCSFNITTSIRDVKQREYALFYKLDVPID--NDNDNTSYRLINCNTSVIT 201
Db |||||
Qy 182 QACPKVSEPIPIHYCTPTGFPALLKCNCKKNGTGPCTNVSTVQCTHGIRPVSTQLL 241
Db |||||
Qy 202 QACPKVSEPIPIHYCTPTGFPALLKCNCKKNGTGPCTNVSTVQCTHGIRPVSTQLL 261
Db |||||
Qy 242 GSLAEVVVIRSENFTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWVTTGEIL 301
Db |||||
Qy 262 GSLAEVVVIRSENFTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWVTTGEIL 321
Db |||||
Qy 302 GNIRQAHCNISRAQWNTLQOIATTLREQFG-NKTIATFNQSSGGDPEIVMHSFNCGGFF 360
Db |||||
Qy 322 GDIRQAVCNLSRTKWDNLKQIVRKLEQFGYGNKTIIVFNHSSGGDPEIVMHSFNCGGFF 381
Db |||||
Qy 361 YCNSTOLFNSANVTSGTW-----SVTRKQKDTGDIITLPCRKQIINRWQVVGKAMYA 415
Db |||||
Qy 382 YCNSTOLFNSANVTSGTW-----SVTRKQKDTGDIITLPCRKQIINRWQVVGKAMYA 439
Db |||||
Qy 416 LPTKGLIRCSSNITGLLTRDGGNGE-NOTTEIFRPGGDMRDNRSELYKYKVKVIEPLG 474
Db |||||
Qy 440 PPIRQIRCSSNITGLLTRDGGNGSRTEIFRPGGDMRDNRSELYKYKVKVIEPLG 499
Db |||||
Qy 475 VAPTKAKRRVQREKRAVGMFLGAMFLGFLGAAGSTMGATSMALTVOARQLLSGIVQQNN 534
Db |||||
Qy 500 VAPTKAKRRVQREKRAVGMFLGAMFLGFLGAAGSTMGASMTLTVOARQLLSGIVQQNN 559
Db |||||
Qy 535 LLRAIKAOQHLLQLTWTGKIQLOARILAVERYLKDQQLLGFPGWCSGKLCITTAVPWNASW 594
Db |||||
Qy 560 LLRAIEAQHLLQLTWTGKIQLOARILAVERYLKDQQLLGFPGWCSGKLCITTVPNWNASW 619
Db |||||
Qy 595 SNKTLDOIWNMTWMEDEIDNYTHLYTLIEESQNOQKQOELLQLDKWSL 649
Db |||||
Qy 620 SNRSLDDIWHNMTWQWEREIDNYTHLYTLIEESQNOQKQOELLQLDKWSL 674
Db |||||

RESULT 13
Q6UYPL_9HIV1

Q6UYPI_9HIV1 PRELIMINARY; PRT; 867 AA.

Q6UYPI; 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Envelope glycoprotein (Fragment)

GN Name-env;

OS Human immunodeficiency virus 1.

OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;

OC Lentivirus; Primate lentivirus group.

OX NCBI_TaxID=11676;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX PubMed=1490899; DOI=10.1128/JVI.78.6.2790-2807.2004;

RA Kuhmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L.,

RA Strick J., Strick J., Riley J., Baroud B.M., Wilson I.A.,

RA Korber B.T., Wolinsky S.M., Moore J.P.;

RT "Genetic and phenotypic analyses of human immunodeficiency virus type 1 escape from a small-molecule CCR5 inhibitor.";

RL J. Virol. 78:2790-2807(2004).

DR EMBL; AY357550; AAR00904.1; -; Genomic_DNA.

DR HSSP; P04578; 1K33.

DR SMR; G6UYPI; 93-147, 209-511, 559-645.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000328; Env GP41.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

KW AIDS; Envelope protein; Transmembrane.

FT NON TER 1

SQ SEQUENCE 867 AA; 98541 MW; F14F0B3372EC7C6D CRC64;

Query Match 83.3%; Score 2892.5; DB 2; Length 867;

Best Local Similarity 83.1%; Pred. No. 1.6e-220;

Matches 545; Conservative 44; Mismatches 52; Indels 15; Gaps 8;

Qy 2 NLWTVYGVVPWKAEATTLFCASDAKAYDEAHNVWATHACVPTNPQVLENTEN 61

Db 40 NLWTVYGVVPWKAEATTLFCASDAKAYDEAHNVWATHACVPTNPQVLENTEN 99

Qy 62 FNMKNVNVQMHEDIISLWDSKPCVKLPCLVTLNCTDLN-TNNNTTTELSTIVV 120

Db 100 FNMKNVNVQMHEDIISLWDSKPCVKLPCLVTLNCTDKNTNNATNTNS----SW 154

Qy 121 -EQRGKGMRCNSFNITTSIRDKVOREYALFYKLDVEPIDDKNTTNTKRLINCNTSV 179

Db 155 GEPMEKGKNCNSFNITTSIRDKVOREYALFYKLDVEPIDDKNTTNTKRLINCNTSV 214

Qy 180 ITQACPKVSEPIPIHYCTPTGFALLKCNCKKFGTGTCTNVSTVQCTHGRPVVSTQLL 239

Db 215 ITQACPKVSEPIPIHYCAPAGFALLKCNCKKFGTGTCTNVSTVQCTHGRPVVSTQLL 274

Qy 240 LNSLAEEVVRSENFTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGE 299

Db 275 LNSLAEEVVRSENFTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGE 334

Qy 300 ILGNIRQAHNCISRAQWNTLQOATTLREOFG-NKTIAFNQSOGDDEIVHNSFCGGE 358

Db 335 IIGDIRKAHCNISRAQWNTLKHVEKLGQFGNNKTIIVFNHSSGGDDEIVHNSFCGGE 394

Qy 359 PFYCNSTOLFNSANVTSGTW--SVTRKQKDTGDIITLPCRIKOINRWQVCKMYAL 416

Db 395 PFYCNSTOLFNSANVTSGTW--SVTRKQKDTGDIITLPCRIKOINRWQVCKMYAL 453

Qy 417 PIKGLIRCSSNITGLLLTRDGGEGNOT---TEIFRPGGDMRDNRWSELYKYKVVKEPL 473

Db 454 PIKGLIRCSSNITGLPLTRDGGEGNOT---TEIFRPGGDMRDNRWSELYKYKVVKEPL 513

Qy 474 GVAPTKAKRVVQREKRAVGLGAMFLGFLGAAGSTMGATSMALTVQARLLSGIVQOQN 533

Db 514 GVAPTKAKRVVQREKRAVGLGAMFLGFLGAAGSTMGATSMALTVQARLLSGIVQOQN 572

Qy 534 NLLRAIKAQOHLLOLTWVGINKQLOARILAVERYLKQOLLGFWGCSGKLICTTAVPWNAS 593

Db 573 NLLRAIKAQOHLLOLTWVGINKQLOARILAVERYLRDQOLLGFWGCSGKIICTTAVPWNAS 632

Qy 594 WSNKTLDOINWNTMMEWDREIDNYTHLYTLIESONQOEKNOELLQLDKWL 649

Db 633 WSNKSMDEINWNTMMEWEKEIDNYTGLIYNLLEKSONQOEKNOELLQLDKWL 688

RESULT 14

Q52S58_9HIV1 PRELIMINARY; PRT; 851 AA.

AC Q52S58;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

DE Envelope glycoprotein.

OS Human immunodeficiency virus 1.

OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;

OC Lentivirus; Primate lentivirus group.

OX NCBI_TaxID=11676;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=H434;

RA Geels M.J., Jansen C., Baan E., De Cuyper I.M., van Schijndel G.J.M.,

RA Pollakis G., Schuitemaker H., Bakker M., Goudamit J., van Baarle D.,

RA Paxton W.A., Miedema F.;

RT "Differential loss of human immunodeficiency virus type 1 (HIV-1) - specific T-helper responses in two HIV-1 infected individuals following CTL escape.";

RT Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY970947; AAX86729.1; -; Genomic_DNA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

KW AIDS; Envelope protein; Transmembrane.

SQ SEQUENCE 851 AA; 96407 MW; A447B60789932CF7 CRC64;

Query Match 83.2%; Score 2890.5; DB 2; Length 851;

Best Local Similarity 83.5%; Pred. No. 2.2e-220;

Matches 550; Conservative 35; Mismatches 35; Indels 39; Gaps 9;

Qy 3 LWTVYGVVPWKAEATTLFCASDAKAYDEAHNVWATHACVPTNPQVLENTENF 62

Db 33 LWTVYGVVPWKAEATTLFCASDAKAYDEAHNVWATHACVPTNPQVLENTENF 92

Qy 63 NMWKNVNVQMHEDIISLWDSKPCVKLPCLVTLNCTDLN-TNNNTTTELSTIVV 119

Db 93 NMWKNVNVQMHEDIISLWDSKPCVKLPCLVTLNCTDLN-TNNNTTTELSTIVV 148

Qy 120 WEORGKGMRCNSFNITTSIRDKVOREYALFYKLDVEPIDDKNTTNTKRLINCNTSV 179

Db 149 WGE-----EMTNCNSFNITTSIRDKVOREYALFYKLDVEPID--KNT---TKRLINCNTSV 199

Qy 180 ITQACPKVSEPIPIHYCTPTGFALLKCNCKKFGTGTCTNVSTVQCTHGRPVVSTQLL 239

Db 200 ITQACPKVSEPIPIHYCTPTGFALLKCNCKKFGTGTCTNVSTVQCTHGRPVVSTQLL 259

Qy 240 LNSLAEEVVRSENFTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGE 299

Db 260 LNSLAEEVVRSENFTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGE 319

Qy 300 ILGNIRQAHNCISRAQWNTLQOATTLREOFGNKTIAFNQSOGDDEIVHNSFCGGEF 359

Db 320 IIGDIRKAHCNISRAQWNTLKHVEKLGQFGNNKTIIVFNHSSGGDDEIVHNSFCGGEF 379

Qy 360 FYCNSTOLFNSANVTSGTW--SVTRKQKDTGDIITLPCRIKOINRWQVCKMYAL 411

Db 380 FYCNSTOLFNSANVTSGTW--SVTRKQKDTGDIITLPCRIKOINRWQVCKMYAL 425

Qy 412 AMYALPIKGLIRCSSNITGLLLTRDGGEG-NQTEIFRPGGDMRDNRWSELYKYKVVKI 470

Db 426 AMYALPIKGLIRCSSNITGLLLTRDGGEG-NQTEIFRPGGDMRDNRWSELYKYKVVKI 485

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Qy 471 EPLGVAPTKARRVYVQREKRAVGMGLGAMFLGAGSTMGATSMALTVOARQLLSGIVQ 530
Db 486 EPLGVAPTKARRVYVQREKRAVGTIGAMFLGAGSTMGAAVALTVQARQLLSGIVQ 545
Qy 531 QONNLLRAIKAAQHLQLTGWGIKQARILAVERYLKDQQLGFWGCGSKLICTTAVPW 590
Db 546 QONNLLRAIEAQHLLQLTGWGIKQARILAVERYLKDQQLGFWGCGSKLICTTAVPW 605
Qy 591 NASNSKTLQIQNNMTWMEWDREIDNYTHLYTLIESQOQEKNOQELLQDKWASL 649
Db 606 NASNSKSLKINWNTWMEWEREIENTSYLIYTLIEPQOQEKNEQELLEDKWASL 664

RESULT 15
Q6UVN6_9HIV1 PRELIMINARY; PRT; 865 AA.
AC Q6UVN6_9HIV1 PRELIMINARY; PRT; 865 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;
RA Kuhnman S.E., Pugach P., Kunatman K.J., Taylor J., Stanfield R.L.,
RA Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
RA Korber B.T., Wolinsky S.M., Moore J.P.;
RT "Genetic and phenotypic analyses of human immunodeficiency virus type
RT 1 escape from a small-molecule CCR5 inhibitor.";
RL J. Virol. 78:2790-2807(2004).
DR EMBL; AY357555; AAR00909.1; -; Genomic_DNA.
DR SMR; Q6UVN6; 93-147, 557-643.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; P: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON_TER
SQ SEQUENCE 865 AA; 98421 MW; 9CB631053888C207 CRC64;
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Query Match 83.2%; Score 2889.5; DB 2; Length 865;
Best Local Similarity 83.0%; Pred. No. 2.7e-220;
Matches 543; Conservative 46; Mismatches 52; Indels 13; Gaps 8;

Qy 2 NLWTVYVYGVPMKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPNOEVVLNVNTE 61
Db 40 NLWTVYVYGVPMKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPNOEVVLNVNTE 99
Qy 62 FNMWKNMVEQMHEDIISLDQSLKPCVKLTPLCVTLNCTDLN-TNNTNTTSLSIIVW 120
Db 100 FNMWKNMVEQMHEDIISLDQSLKPCVKLTPLCVTLNCTDLN-TNNTNTTSLSIIVW 154
Qy 121 -EQRGKGMENCSFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCVTSV 179
Db 155 GEPMEKEIKNCSFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCVTSV 214
Qy 180 ITQACPKVSEPIPIHYCTPTGFALLKCNDFKNGTGPCTNVSTVQCTHGIRPWSQTLL 239
Db 215 ITQACPKVSEPIPIHYCAPAGFALLKCNDFKNGTGPCTNVSTVQCTHGIRPWSQTLL 274
Qy 240 LNSGLAEVEVIRSENFNTNAKIIIVQLNVSVSEINCTRPNNHTRKRVTLGPGRVWYTTGE 299
Db 275 LNSGLAEKEVIRSENFNTNAKIMVQLNVSVSEINCTRPNNHTRKRVTLGPGRVWYTTGE 334
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Db 335 IIGDIRKAHCNISRAQNNNTLKHIVEKLGKQFGNNKTIIVENHSSGGDPEIVMHSFNCGGE 394
Qy 359 PFCNSTQLPNSAWNTVTSNGTSV--TRKQKDTGDIITLPCRKQIINRWQVVGKAMYAL 416
Db 395 PFCNSTKLFPNSTW-TRKNGTWTNPDTERSNSTEETHITLPCRKQIINRWQVVGKAMYAP 453
Qy 417 PIKGLIRCSSNITGLLLTRDGGGENOT-TFIFRPGGDMRDNRSELYKYKVKVIBPLGV 475
Db 454 PIKGLIRCSSNITGLLLTRDGGNNDTSGTEIFRPGGDMRDNRSELYKYKVKVIBPLGI 513
Qy 476 APTKAKRRVYVQREKRAVGMGLGAMFLGAGSTMGATSMALTVOARQLLSGIVQOQNNL 535
Db 514 APTKAKRRVYVQREKRAVG-IGAMFLGAGSTMGASVTLTVQARQLLSGIVQOQNNL 572
Qy 536 LRAIKAQHLLQLTGWGIKQARILAVERYLKDQQLGFWGCGSKLICTTAVPWNASWS 595
Db 573 LRAIEAHQHLQLTGWGIKQARVLAVERYLKDQQLGFWGCGSKLICTTAVPWNASWS 632
Qy 596 NKTLDOIWNMTWMEWDREIDNYTHLYTLIESQOQEKNOQELLQDKWASL 649
Db 633 NKSMDEIWNMTWMEWEKEIDNYTGLIYNLLEKSNQOQEKNEQELLQDKWANL 686
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Search completed: March 7, 2006, 17:50:37
Job time : 299.698 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 7, 2006, 17:51:03 ; Search time 67.9631 Seconds
(without alignments)
789.495 Million cell updates/sec

Title: US-09-938-406-1_COPY_33_681
Perfect score: 3474
Sequence: 1 ANLWTVYGVVWKEATT.....QNOQKNOQLLODKWASL 649

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2883.5	83.0	847	2	US-09-476-242-2
2	2852	82.1	850	1	US-08-448-603A-28
3	2852	82.1	850	2	US-09-134-075-28
4	2852	82.1	850	2	US-09-492-739-28
5	2852	82.1	850	2	US-09-966-931A-28
6	2834	81.6	855	1	US-08-022-835-6
7	2834	81.6	855	1	US-08-388-809-6
8	2834	81.6	855	1	US-08-647-714-6
9	2827.5	81.4	843	2	US-09-602-864-13
10	2818	81.1	855	2	US-07-956-483-14
11	2814.5	81.0	826	1	US-08-375-510-2
12	2814.5	81.0	826	1	US-08-487-657-2
13	2814.5	81.0	854	2	US-09-309-572-23
14	2814.5	81.0	854	2	US-09-718-096-23
15	2814	81.0	880	1	US-08-788-815-7
16	2814	81.0	880	2	US-09-157-963-7
17	2814	81.0	880	2	US-09-568-105-7
18	2809.5	80.9	856	1	US-07-916-098A-2
19	2809.5	80.9	856	1	US-09-476-242-1
20	2809.5	80.9	857	1	US-08-448-603A-30
21	2809.5	80.9	857	2	US-09-134-075-30
22	2809.5	80.9	857	2	US-09-492-739-30
23	2809.5	80.9	857	2	US-09-966-931A-30
24	2807.5	80.8	855	2	US-07-956-483-15
25	2806.5	80.8	856	2	US-09-124-900-9
26	2806.5	80.8	863	2	US-08-463-210-11
27	2806.5	80.8	863	2	US-08-463-028-11

28 2806.5 80.8 863 2 US-08-463-209-11 Sequence 11, Appl
29 2795.5 80.5 856 2 US-09-337-387-11 Sequence 11, Appl
30 2795.5 80.5 856 2 US-10-196-515-11 Sequence 11, Appl
31 2795 80.5 861 1 US-08-127-499A-14 Sequence 14, Appl
32 2795 80.5 861 1 US-08-482-847-14 Sequence 14, Appl
33 2795 80.5 861 2 US-07-956-483-10 Sequence 10, Appl
34 2795 80.5 861 2 US-08-472-240A-1 Sequence 7, Appl
35 2795 80.5 861 2 US-08-472-240A-7 Sequence 1, Appl
36 2795 80.5 861 2 US-08-817-441-103 Sequence 103, App
37 2787 80.2 861 2 US-07-956-483-16 Sequence 16, Appl
38 2786.5 80.2 865 2 US-07-956-483-13 Sequence 13, Appl
39 2781.5 80.1 887 2 US-08-472-240A-5 Sequence 5, Appl
40 2781 80.1 665 1 US-08-448-603A-32 Sequence 32, Appl
41 2781 80.1 665 2 US-09-134-075-32 Sequence 32, Appl
42 2781 80.1 665 2 US-09-492-739-32 Sequence 32, Appl
43 2781 80.1 665 2 US-09-966-931A-32 Sequence 32, Appl
44 2780 80.0 657 2 US-09-256-194-2 Sequence 2, Appl
45 2772 79.8 635 2 US-09-536-977-68 Sequence 68, Appl

ALIGNMENTS

RESULT 1

US-09-476-242-2
; Sequence 2, Application US/09476242
; Patent No. 6689879
; GENERAL INFORMATION:
; APPLICANT: BARNETT, Susan
; APPLICANT: HARTOG, Karin
; APPLICANT: MARTIN, Eric
; TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
; FILE REFERENCE: 1605.002
; CURRENT APPLICATION NUMBER: US/09/476.242
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 847
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-476-242-2

Query Match 83.0%; Score 2883.5; DB 2; Length 847;
Best Local Similarity 83.3%; Pred. No. 1.5e-229;
Matches 544; Conservative 40; Mismatches 38; Indels 31; Gaps 7;
Qy 3 LWTVYGVVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 62
Db 33 LWTVYGVVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 92
Qy 63 NMWKNVVEQMHEDIISLDOSLKPCKVLTPLCVTLNCTDLNNTNTTNTTSLIIVVWEQ 122
Db 93 NMWKNVVEQMHEDIISLDOSLKPCKVLTPLCVTLNCTDLNNTNTKSSN----WKE 146
Qy 123 RGKEMRNCSPNITTSIRDKVQREYALFYKLDVDPIDNKNNTNTNTKYLNCNNTSVITQ 182
Db 147 MDRGEIKNCSPKVTTSIRNKQKEYALFYKLDVVPIDN-----DNTSYKLNCTSVITQ 201
Qy 183 ACPKVSPEPIPIHYCTPTGTFALLKCNKDKNGTGFCTNVTQCTHGRPVVSTQILLNG 242
Db 202 ACPKVSPEPIPIHYCAPAGFAILLKCNKDKNGTGFCTNVTQCTHGRPVVSTQILLNG 261
Qy 243 SLAEEVVRSENNNAKTIIVQLNVSVEINCTRNPNHTKRVTLGPRVWYTTGILG 302
Db 262 SLAEEVVRSENNFTDAKTIIVQLKESVEINCTRNPNHTKRVTLGPRVWYTTGILG 321
Qy 303 NIRAHCNISRQWNTLQIATTLRQFGNKTIAFNQSSGGDPEIVHNSFCGGEFFYC 362
Db 322 DIRQHCNISGEKNWNTLKQIVTKLQAFQGNKTIVFKQSSGGDPEIVHNSFCGGEFFYC 381
Qy 363 NSTOLFNSAMVNT-----SNGTWSVTRKQKDTGDIITLPCRIKQIINRWVGVKAMVALP 417

Db 382 NSTQLFNSNTWNTGPNNTNGT-----ITLPCRIKQIINRWQVGVKAMYAPP 428
Qy 418 IKGLIRCSNITGLLLTRDGGGE-NQTTTEIFRPGGDMRDNRSELYKYKVKVIEPLGVA 476
Db 429 IRGQIRCSNITGLLLTRDGGGEISNTTEIFRPGGDMRDNRSELYKYKVKVIEPLGVA 488
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Qy 537 RAIKAAQHLLQLTWVGIIKQARILAVERYLKDOQLLGFWCGSGKLICTTAVPWNASWSN 596
Db 548 RAIKAAQHLLQLTWVGIIKQARILAVERYLKDOQLLGFWCGSGKLICTTAVPWNASWSN 607
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Db 608 KSLDOQNNMTWMEWDREIDNTHLYTLIESQOQEKNEQELLELDKQWASL 660

RESULT 2
US-08-448-603A-28
; Sequence 28, Application US/08448603A
; Patent No. 5864027
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; APPLICANT: Nakamura, Gerald R.
; TITLE OF INVENTION: HIV Envelope Polypeptides
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP
; STREET: 3 Embarcadero Center
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,603A
; FILING DATE: 07-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/072,833
; FILING DATE: 07-JUN-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Haliday, Emily
; REGISTRATION NUMBER: 38903
; REFERENCE/DOCKET NUMBER: 14918-704
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-393-2000
; TELEFAX: 415-393-2286
; TELEX:
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 850 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-448-603A-28

Query Match 82.1%; Score 2852; DB 1; Length 850;
Best Local Similarity 83.0%; Pred. No. 6.2e-227;
Matches 537; Conservative 42; Mismatches 52; Indels 16; Gaps 7;

Qy 3 LWTVVYGVFWKATTTTLFCASDAKAYDTFAHNVWATHACVPTNPNPQEVLENVTENF 62
Db 33 LWTVVYGVFWKATTTTLFCASDAKAYDTFAHNVWATHACVPTNPNPQEVLENVTENF 92
Qy 63 NMWKNMVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDL--KNAINTTSSS-----WGK 146

Db 93 NMWKNMVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDL--KNAINTTSSS-----WGK 146
Qy 123 RGKEMENCSPNITTSIRDKVQREYALFYKLDVPEIDNKNNTNTNTKYRLINCNTSVITQ 182
Db 147 MERGEIKNCSFNVTTSIRDKMNEYALFYKLDVVVIDN-----DNTSYRLISCNTSVITQ 201
Qy 183 ACPRVSPPEPIPIHYCTPTGFPALLKCNCKENGCTGCTNVTVOCTHGRPVVSTQLLNG 242
Db 202 ACPRVSPPEPIPIHYCAPAGFALLKCRDKKFNCTGCTNVTVOCTHGRPVVSTQLLNG 261
Qy 243 SLAEEVVIRSENFTNNAKTIIVOLNVSEINCTRPNNHTRKRVTLGPRVWYTTGILG 302
Db 262 SLAEEVVIRSANFSDNAKTIIVOLNESVEINCTRPNNHTRRSIHIGRAFYATGIIIG 321
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Db 322 DIRQAHNCNLSTKWNNTLKQIVTKLREHF-NKTIIVFNHSSGGDPEIWMHSPNCGGEFFYC 380
Qy 363 NSTOLFNSAWNVTSGTWSVTRKQKOTGDIITLPCRIKQIINRWQVGVKAMYALPIKGLI 422
Db 381 NTPPLFNSTWNTYV--TWNTEGSDNIGRNTLQCRKQIINNMQEVGKAMYPPIRGQI 438
Qy 423 RCSSNITGLLLTRDGGGENQTTTEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPTAKR 482
Db 439 RCSSNITGLLLTRD-GGNNSETEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPTAKR 497
Qy 483 RVVQREKRAVGMFLGAMFLGFLGAAGSTMGATSMALTVOARQLLSGIVQOQNLLRAKQ 542
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Qy 543 QHLLQLTWVGIIKQARILAVERYLKDOQLLGFWCGSGKLICTTAVPWNASWSNKTLDQI 602
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Qy 603 WNNMTWMEWDREIDNTHLYTLIESQOQEKNOQELLDKQWASL 649
Db 617 WNNMTWMEWDREIDNTHLYTLIESQOQEKNEQELLELDKQWASL 663

RESULT 3
US-09-134-075-28
; Sequence 28, Application US/09134075
; Patent No. 6042836
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; APPLICANT: Nakamura, Gerald R.
; TITLE OF INVENTION: HIV Envelope Polypeptides
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP
; STREET: 3 Embarcadero Center
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,075
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,603
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haliday, Emily
; REGISTRATION NUMBER: 38903
; REFERENCE/DOCKET NUMBER: 14918-704
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-393-2000

```

; TELFAX: 415-393-2286
; TELEX:
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 850 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-134-075-28

Query Match      82.1%; Score 2852; DB 2; Length 850;
Best Local Similarity 83.0%; Pred. No. 6.2e-227;
Matches 537; Conservative 42; Mismatches 52; Indels 16; Gaps 7;

QY 3 LWTYYGVVWKEATTLFCASDAKAYDTEAHNVWATHACVPNPNPQEVVLENVTNF 62
DB 33 LWTYYGVVWKEATTLFCASDAKAYDTEAHNVWATHACVPNPNPQEVVLENVTNF 92
QY 63 NMKNMVEQWHEDIISLDQSLKPCVKLTPLCVTLNCTDLTNTNTTSLIIVVWEQ 122
DB 93 NMKNMVEQWHEDIISLDQSLKPCVKLTPLCVTLNCTDLTNTNTTSSS-----WGK 146
QY 123 RGKGMNCSFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYLINCNMTSVITQ 182
DB 147 MERGEIKNCSFNVTTSIRDKMNEVALFYKLDVVIDN-----DNTSYRLISCNMTSVITQ 201
QY 183 ACPKVSPEPIPIHYCTPTGPFALLKNDCKFNGTGPCTNVSTVQCTHGIPIVSTQLLNG 242
DB 202 ACPKVSPEPIPIHYCAPAGFAILKCRDKKFGTGPCTNVSTVQCTHGIPIVSTQLLNG 261
QY 243 SLAEVYVIRSENFNTNNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPRVWYTTGILG 302
DB 262 SLAEVYVIRSENFNTNNAKTIIVQLNVSVEINCTRPNNHTRSHIGGRAFYATGILG 321
QY 303 NIQAHCNISRQWNTLQIATTLREOFNGKTIATFNOSSGGDPEIWMHSENCGBEPYC 362
DB 322 DIRQAHCLSTKNNTLKQIVTKLREHF-NKTIIVFNHSSGGDPEIWMHSENCGBEPYC 380
QY 363 NSTQFNSAMNVTSGTWSVTRKQKDTGDIITLPCRIKQIINRWQVVGKAMYPALPIKGLI 422
DB 381 NTPLEFNSWTNVTY--TWNTEGSDTGRNITLQCRKQIINMWQVVGKAMYPALPIRQOI 438
QY 423 RCSSNITGLLTRDGGGNGOTTEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPTAKR 482
DB 439 RCSSNITGLLTRD--GGNSETEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPTAKR 497
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DB 498 RVVQREKRAVG-IGAVFLGFLGAAGSTMGTATSMALTVQARQLLSGIIVQQNNLLRAIEAE 556
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DB 557 QHLLQLTWGIGIKQLQARILAVERYLKQQLLGFWGCCKLICTTAVPWNASWSNKSIDKI 616
QY 603 WNNMTWEDREIDNTHLYITLIEESQOQEKQQLLDKQWASL 649
DB 617 WDNMTWEDREIDNTHLYITLIEESQOQEKQQLLDKQWASL 663

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RESULT 4

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US-09-492-739-28
; Sequence 28, Application US/09492739
; Patent No. 6331404
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; INVENTOR: Nakamura, Gerald R.
; TITLE OF INVENTION: HIV Envelope Polypeptides
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP
; STREET: 3 Embarcadero Center
; CITY: San Francisco
; STATE: CA

```

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; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/492.739
; FILING DATE: 27-Jan-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/134,075
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Haliday, Emily
; REGISTRATION NUMBER: 38903
; REFERENCE/DOCKET NUMBER: 14918-704
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-393-2000
; TELEFAX: 415-393-2286
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 850 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-492-739-28

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Query Match      82.1%; Score 2852; DB 2; Length 850;
Best Local Similarity 83.0%; Pred. No. 6.2e-227;
Matches 537; Conservative 42; Mismatches 52; Indels 16; Gaps 7;

QY 3 LWTYYGVVWKEATTLFCASDAKAYDTEAHNVWATHACVPNPNPQEVVLENVTNF 62
DB 33 LWTYYGVVWKEATTLFCASDAKAYDTEAHNVWATHACVPNPNPQEVVLENVTNF 92
QY 63 NMKNMVEQWHEDIISLDQSLKPCVKLTPLCVTLNCTDLTNTNTTSLIIVVWEQ 122
DB 93 NMKNMVEQWHEDIISLDQSLKPCVKLTPLCVTLNCTDLTNTNTTSSS-----WGK 146
QY 123 RGKGMNCSFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTNTKYLINCNMTSVITQ 182
DB 147 MERGEIKNCSFNVTTSIRDKMNEVALFYKLDVVIDN-----DNTSYRLISCNMTSVITQ 201
QY 183 ACPKVSPEPIPIHYCTPTGPFALLKNDCKFNGTGPCTNVSTVQCTHGIPIVSTQLLNG 242
DB 202 ACPKVSPEPIPIHYCAPAGFAILKCRDKKFGTGPCTNVSTVQCTHGIPIVSTQLLNG 261
QY 243 SLAEVYVIRSENFNTNNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPRVWYTTGILG 302
DB 262 SLAEVYVIRSENFNTNNAKTIIVQLNVSVEINCTRPNNHTRSHIGGRAFYATGILG 321
QY 303 NIQAHCNISRQWNTLQIATTLREOFNGKTIATFNOSSGGDPEIWMHSENCGBEPYC 362
DB 322 DIRQAHCLSTKNNTLKQIVTKLREHF-NKTIIVFNHSSGGDPEIWMHSENCGBEPYC 380
QY 363 NSTQFNSAMNVTSGTWSVTRKQKDTGDIITLPCRIKQIINRWQVVGKAMYPALPIKGLI 422
DB 381 NTPLEFNSWTNVTY--TWNTEGSDTGRNITLQCRKQIINMWQVVGKAMYPALPIRQOI 438
QY 423 RCSSNITGLLTRDGGGNGOTTEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPTAKR 482
DB 439 RCSSNITGLLTRD--GGNSETEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPTAKR 497
QY 483 RVVQREKRAVGMGLGAMFLGFLGAAGSTMGTATSMALTVQARQLLSGIIVQQNNLLRAIKAO 542
DB 498 RVVQREKRAVG-IGAVFLGFLGAAGSTMGTATSMALTVQARQLLSGIIVQQNNLLRAIEAE 556
QY 543 QHLLQLTWGIGIKQLQARILAVERYLKQQLLGFWGCCKLICTTAVPWNASWSNKTLDQI 602

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Db 557 QHLLQLTVWGIKOQARVLAVERYLKDQQLLGGWCGSKLICCTTAVPWNASWNSKSLDKI 616
Qy 603 WNNMTWMEWDREIDNTHLYTLIEESQOQKNOQELLQDKWASL 649
Db 617 WDNMTWMEWEREIDNTHLYTLIEESQOQKNOQELLQDKWASL 663

RESULT 5
US-09-966-931A-28
; Sequence 28, Application US/09966931A
; Patent No. 6806055
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; Nakamura, Gerald R.
; TITLE OF INVENTION: HIV Envelope Polypeptides
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP
; STREET: 3 Embarcadero Center
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/966,931A
; FILING DATE: 27-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/492,739
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Haliday, Emily
; REGISTRATION NUMBER: 38903
; REFERENCE/DOCKET NUMBER: 14918-704
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-393-2000
; TELEFAX: 415-393-2286
; TEXT: <Unknown>
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 850 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-966-931A-28

Query Match 82.1%; Score 2852; DB 2; Length 850;
Best Local Similarity 83.0%; Pred. No. 6.2e-227;
Matches 537; Conservative 42; Mismatches 52; Indels 16; Gaps 7;

Qy 3 LWTVVYGVVPWKEATTTLCASDAKAYDTEAHNVWATHACVTPNPQEVLENVTENF 62
Db 33 LWTVVYGVVPWKEATTTLCASDAKAYDTEAHNVWATHACVTPNPQEVLENVTENF 92
Qy 63 NMWKNNVQOMHEDIISLQSLKPCVKLTPLCVTLNCTDLNNTNTTSLSIIVVWEQ 122
Db 93 NMWKNNVQOMHEDIISLQSLKPCVKLTPLCVTLNCTDLNNTNTTSSS-----WGK 146
Qy 123 RGKGMENCSFNITTSIRDKVQREYALFYKLDVEPIDDKNNTNTNTKYRLINCNTSVITQ 182
Db 147 MERGEIKNCSENVVTSIRDKMNEYALFYKLDVVPIDN-----DNTSYRLISCNTSVITQ 201
Qy 183 ACPKVSPEPIPIHYCTPTGTFALLKCNCKNGKNGTGTNNVSTVQCTGTHGIRPVWSTQLLNG 242
Db 202 ACPKVSPEPIPIHYCAPAGFAILKCRDKFKNGTGTNNVSTVQCTGTHGIRPVWSTQLLNG 261
Qy 243 SLAEVEVWIRSENFNTNNAKTIIVQLNVSVSEINCTRPNNHTKRVTGLGPRVWVYTTGILG 302

Db 262 SLAEVEVWIRSENFNTNNAKTIIVQLNVSVSEINCTRPNNHTKRVTGLGPRVWVYTTGILG 321
Qy 303 NTRQAHNCNISRQWNNNTLOQIATTLREQFGNKTIAFNQSSGGDPETVMSFNCGGFFCYC 362
Db 322 DIRQAHNCNLSSTKWNNTLKQIVTKLREHF-NKTIIVFNHSSGGDPETVMSFNCGGFFCYC 380
Qy 363 NSTQLFNSAWNVTSTNGTWSVTRKQKDTGDIITLPCRIKQIINRWQVVGKAMVALPIKGLI 422
Db 381 NTPPLFNSTWNYTY--TWNTGSDNTGRNITLQCHIKQIINMWQEVGKAMVAPPVIRGOI 438
Qy 423 RCSSNITGLLLTRDGGGNGOTTEIFRPGGDMRDNRSELYKYKVKVIBPLGVAPTKAKR 482
Db 439 RCSSNITGLLLTRD-GGNNSETEIFRPGGDMRDNRSELYKYKVKVIBPLGVAPTKAKR 497
Qy 483 RVVOREKRAVGMFLGAMFLGAGSTMGATSMALTVAQRLLSGLVQOONLLRAIKAQ 542
Db 498 RVNOREKRAVG-IGAVFLGFLGAGSTMGAASTVTLTVAQRLLSGLVQOONLLRAIEAE 556
Qy 543 QHLLQLTVWGIKOQARVLAVERYLKDQQLLGGWCGSKLICCTTAVPWNASWNSKSLDKI 602
Db 557 QHLLQLTVWGIKOQARVLAVERYLKDQQLLGGWCGSKLICCTTAVPWNASWNSKSLDKI 616
Qy 603 WNNMTWMEWDREIDNTHLYTLIEESQOQKNOQELLQDKWASL 649
Db 617 WDNMTWMEWEREIDNTHLYTLIEESQOQKNOQELLQDKWASL 663

RESULT 6
US-08-022-835-6
; Sequence 6, Application US/08022835
; Patent No. 5420030
; GENERAL INFORMATION:
; APPLICANT: Reitz Jr., Marvin S.
; APPLICANT: Franchini, Genoveffa
; APPLICANT: Markham, Phillip D.
; APPLICANT: Gallo, Robert C.
; APPLICANT: Lori, Franco C.
; APPLICANT: Popovic, Mikulas
; APPLICANT: Garnter, Suzanne
; TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1 AND USES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: Eleventh Floor, 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/022,835
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/599,491
; FILING DATE: 17-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: WTS/5683/78507/SRL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 855 amino acids
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Db 172 ACPKISPEPIPIHYCAPAGPAILKCKNDKTFNGKGPCKNVSVTQCTHGIRPVVSTQLLNG 231
Qy 243 SLAEVVRSENFNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGELG 302
Db 232 SLAEVVRSENFNNAKTIIVQLKESVEINCTRPNNHTRKRVTLGPRVWYTTGELG 291
Qy 303 NIROAHNCISRAQNNNTLQIATTLREOFNGKNTAFNOSGDDPEIVMHSFNCGEFFYC 362
Db 292 DIROAHNCISRAQNNNTLQIATTLREOFNGKNTAFNOSGDDPEIVMHSFNCGEFFYC 351
Qy 363 NSTOLFNSAMVNTSGTWSVTRKQKDTGDIITLPCRIKQIINRWQVGVKAMYPILKGLI 422
Db 352 NSTOLFNSAMVNTSGTWSVTRKQKDTGDIITLPCRIKQIINRWQVGVKAMYPILKGLI 405
Qy 423 RCSSNITGLLTRDGGNGNTTEIFRPGGDMRDNRSELYKYKVKIEPLGVAPTAKR 482
Db 406 RCSSNITGLLTRDGGNGNTTEIFRPGGDMRDNRSELYKYKVKIEPLGVAPTAKR 465
Qy 483 RVQREKAVGMLGMPFLGFGAAGSTMGATSMALTVOARQLLSGIVQOQNNLLRAIKAO 542
Db 466 RVQREKAVG-IGAVFLGFGAAGSTMGATSMALTVOARQLLSGIVQOQNNLLRAIKAO 524
Qy 543 QHLLQTLVWGIKQIARILAVERYLKDQQLGFWGCSGKLICTTAVPWNASWNSKTLDOI 602
Db 525 QHLLQTLVWGIKQIARILAVERYLKDQQLGFWGCSGKLICTTAVPWNASWNSKTLDOI 584
Qy 603 WNNMTWMDREIDNYTHLYTLIEESQOQEKQELLDKRWASL 649
Db 595 WNNMTWMDREIDNYTHLYTLIEESQOQEKQELLDKRWASL 631

RESULT 10

US-07-956-483-14
; Sequence 14, Application US/07956483
; Patent No. 6261799
; GENERAL INFORMATION:
; APPLICANT: KIENY, Marie-Paule
; TITLE OF INVENTION: NOVEL HYBRID, SOLUBLE AND UNCLEAVED
; TITLE OF INVENTION: 5P160 VARIANT
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956,483
; FILING DATE: 31-DEC-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 92/19742
; FILING DATE: 12-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 05392
; FILING DATE: 02-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feuty, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 017753-005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 855 amino acids
; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-956-483-14
Query Match 81.1%; Score 2818; DB 2; Length 855;
Best Local Similarity 81.3%; Pred. No. 4e-224;
Matches 534; Conservative 39; Mismatches 54; Indels 30; Gaps 7;
Qy 3 LWTVYVYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTENF 62
Db 33 LWTVYVYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTENF 92
Qy 63 NMWKNNVVEQMHEDIISLDQSLKPCVKLPLCVTLNCTDLNNTNTTNTTSELSIIVVWEQ 122
Db 93 NMWKNNVVEQMHEDIISLDQSLKPCVKLPLCVTLNCTDLNNTNTTNTTSELSIIVVWEQ 148
Qy 123 RGK---GEMRNCNSNITTSIRSKVOREYALFYKLDVEPIDDKNTYNTKYLNCNTSV 179
Db 149 RGRMEGEMTNCNSNITTSIRSKVOREYALFYKLDVEPIDDKNTYNTKYLNCNTSV 201
Qy 180 ITQACPKVSEPIPIHYCTPTGFAKLLCNDKNGTGTCTNVSTVQCTHGIRPVVSTOLL 239
Db 202 ITQACPKVSEPIPIHYCA-RWFAILNCNNKFKNGTGTCTNVSTVQCTHGIRPVVSTOLL 260
Qy 240 LNSLAEEVVRSENFNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGE 299
Db 261 LNSLAEEVVRSENFNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGE 320
Qy 300 ILGNIROAHNCISRAQNNNTLQIATTLREOFNGKNTAFNOSGDDPEIVMHSFNCGEFF 359
Db 321 IIGDIROAHNCISRAQNNNTLQIATTLREOFNGKNTAFNOSGDDPEIVMHSFNCGEFF 380
Qy 360 FYCNSSTOLFNSAMVNT--SNGTWSVTRKQKDTGDIITLPCRIKQIINRWQVGVKAMYPALP 417
Db 381 FYCNSSTOLFNSAMVNT--SNGTWSVTRKQKDTGDIITLPCRIKQIINRWQVGVKAMYPALP 432
Qy 418 IKGLIRCSSNITGLLTRDGGNGNTTEIFRPGGDMRDNRSELYKYKVKIEPLGVAPTAKR 472
Db 433 IKGLIRCSSNITGLLTRDGGNGNTTEIFRPGGDMRDNRSELYKYKVKIEPLGVAPTAKR 492
Qy 473 LGVAPTAKRVRVQREKAVGMLGMPFLGFGAAGSTMGATSMALTVOARQLLSGIVQOQ 532
Db 493 LGVAPTAKRVRVQREKAVGMLGMPFLGFGAAGSTMGATSMALTVOARQLLSGIVQOQ 552
Qy 533 NNLRAIKAOQHLLQTLVWGIKQIARILAVERYLKDQQLGFWGCSGKLICTTAVPWNAS 592
Db 553 NNLRAIKAOQHLLQTLVWGIKQIARILAVERYLKDQQLGFWGCSGKLICTTAVPWNAS 612
Qy 593 WSNKTLDOIWNMTWMDREIDNYTHLYTLIEESQOQEKQELLDKRWASL 649
Db 613 WSNKTLDOIWNMTWMDREIDNYTHLYTLIEESQOQEKQELLDKRWASL 669

RESULT 11

US-08-375-510-2
; Sequence 2, Application US/08375510
; Patent No. 5576421
; GENERAL INFORMATION:
; APPLICANT: Saito, Atsushi
; APPLICANT: Sinagawa, Hideo
; APPLICANT: Nakata, Atsuo
; TITLE OF INVENTION: HIV ANTIGEN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch and Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,510
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/07/985,949
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 216-309P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
TELEFAX: (703) 241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 826 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-375-510-2

Query Match 81.0%; Score 2814.5; DB 1; Length 826;
Best Local Similarity 82.9%; Pred. No. 7.4e-224;
Matches 540; Conservative 34; Mismatches 56; Indels 21; Gaps 9;

Qy 3 LWTVYGVVPWKAEATTLFCASDAKAYDTEAHNVWATHACVPTNPQVVLNVTFENF 62
Db 6 LWTVYGVVPWKAEATTLFCASDAKAYDTEAHNVWATHACVPTNPQVVLNVTFENF 65
Qy 63 NMWKNVVEQMHEDIISLWDSKPCVKLTPLCVTLNCTDLNNTNTTNTTSLSIIVVEQ 122
Db 66 NMWKNVVEQMHEDIISLWDSKPCVKLTPLCVTLNCTDLNNTNTSSSGRMTIME- 122
Qy 123 RGKGMKNCNFNTTSIRDKVQREYALFYKLDVEPIDDKNNTNTKYRLINCNTSVITQ 182
Db 123 --KGETKNCNFNTTSIRDKVQREYALFYKLDVEPIDDKNNTNTSSSGRMTIME- 173
Qy 183 ACQKVSPEPIPIHYCAPAGFAILCKNNKTFNGTGTCTNVSTVQCTHGIRPVVSTQLLNG 242

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,510
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/07/985,949
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 216-309P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
TELEFAX: (703) 241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 826 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-375-510-2

Query Match 81.0%; Score 2814.5; DB 1; Length 826;
Best Local Similarity 82.9%; Pred. No. 7.4e-224;
Matches 540; Conservative 34; Mismatches 56; Indels 21; Gaps 9;

Qy 3 LWTVYGVVPWKAEATTLFCASDAKAYDTEAHNVWATHACVPTNPQVVLNVTFENF 62
Db 6 LWTVYGVVPWKAEATTLFCASDAKAYDTEAHNVWATHACVPTNPQVVLNVTFENF 65
Qy 63 NMWKNVVEQMHEDIISLWDSKPCVKLTPLCVTLNCTDLNNTNTTNTTSLSIIVVEQ 122
Db 66 NMWKNVVEQMHEDIISLWDSKPCVKLTPLCVTLNCTDLNNTNTSSSGRMTIME- 122
Qy 123 RGKGMKNCNFNTTSIRDKVQREYALFYKLDVEPIDDKNNTNTKYRLINCNTSVITQ 182
Db 123 --KGETKNCNFNTTSIRDKVQREYALFYKLDVEPIDDKNNTNTSSSGRMTIME- 173
Qy 183 ACQKVSPEPIPIHYCAPAGFAILCKNNKTFNGTGTCTNVSTVQCTHGIRPVVSTQLLNG 242

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,510
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/07/985,949
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 216-309P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
TELEFAX: (703) 241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 826 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-487-657-2

Query Match 81.0%; Score 2814.5; DB 1; Length 826;
Best Local Similarity 82.9%; Pred. No. 7.4e-224;
Matches 540; Conservative 34; Mismatches 56; Indels 21; Gaps 9;

Qy 3 LWTVYGVVPWKAEATTLFCASDAKAYDTEAHNVWATHACVPTNPQVVLNVTFENF 62
Db 6 LWTVYGVVPWKAEATTLFCASDAKAYDTEAHNVWATHACVPTNPQVVLNVTFENF 65
Qy 63 NMWKNVVEQMHEDIISLWDSKPCVKLTPLCVTLNCTDLNNTNTTNTTSLSIIVVEQ 122
Db 66 NMWKNVVEQMHEDIISLWDSKPCVKLTPLCVTLNCTDLNNTNTSSSGRMTIME- 122
Qy 123 RGKGMKNCNFNTTSIRDKVQREYALFYKLDVEPIDDKNNTNTKYRLINCNTSVITQ 182
Db 123 --KGETKNCNFNTTSIRDKVQREYALFYKLDVEPIDDKNNTNTSSSGRMTIME- 173
Qy 183 ACQKVSPEPIPIHYCAPAGFAILCKNNKTFNGTGTCTNVSTVQCTHGIRPVVSTQLLNG 242
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Db 174 ACPKVSPEPIPIHYCAPAGFAILKCNKNTFNGTGTCTVSTVQCTHGRPVVSTOLLING 233
Qy 243 SLAEEDVIRSNFTNNAKTIIVQLNVSVINCTRPNNHTRK--RVTLGPGRVWVTTGEBI 300
Db 234 SLAEEDVIRSNFTNNAKTIIVQLNVSVINCTRPNNHTRKSIIRIQPGRAFVTIGKI 293
Qy 301 LGNIROAHCHNISRAQWNTLQOIATTLREOFG-NKTIAPNOSGGDPPIVMSHFNCGGEF 359
Db 294 -GNMROAHCHNISRAQWNTLQOIATTLREOFGNNTIIFKOSGGDPPIVTHSFNCGGEF 352
Qy 360 FYCNSTOLFNSAWNTSNGTWSVTRKQKDTG-DIITLPCRILQIINRWQVVGKAMALPI 418
Db 353 FYCNSTOLFNSW---FNSWSTEGSNNTGSDTITLPCRILQIINRWQVVGKAMALPI 409
Qy 419 KGLIRCSNITGLLLTRDGGGNGOTTEIFRPGGDMRDNRSELYKYKVVKIEPLGVAPT 478
Db 410 SGOIRCSNITGLLLTRDGGGNNNGSEIFRPGGDMRDNRSELYKYKVVKIEPLGVAPT 469
Qy 479 KAKRVVOREKRAVGMFLGFLGAAGSTMGATSMALTVOARQLLSGI VQQNNLLRA 538
Db 470 KAKRVVOREKRAVG-IGALFLGFLGAAGSTMGCTSMTLTVOARQLLSDI VQQNNLLRA 528
Qy 539 IKAQOHLQLTWGILKQIARILAVERYLKQOQLLGFWGC SGKLICTTAVPWNASWSNKT 598
Db 529 IEAQOHLQLTWGILKQIARILAVERYLKQOQLLGFWGC SGKLICTTAVPWNASWSNKS 588
Qy 599 LDQIWNNTMWEWDREINNYTHLYTLIESONQOEKQOQLLQDKWASL 649
Db 589 LEQIWNNTMWEWDREINNYTHLYTLIESONQOEKQOQLLQDKWASL 639

RESULT 13

US-09-309-572-23
; Sequence 23, Application US/09309572
; Patent No. 6440730
; GENERAL INFORMATION:
; APPLICANT: Heinrich-Pette-Institut
; TITLE OF INVENTION: Retroviral hybrid vectors pseudotyped with LCMV
; FILE REFERENCE: P50489
; CURRENT APPLICATION NUMBER: US/09/309,572
; PRIOR FILING DATE: 1999-05-11
; EARLIER APPLICATION NUMBER: DE 198 56 463
; EARLIER FILING DATE: 1998-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 854
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: envelope polyprotein
US-09-309-572-23

Query Match 81.0%; Score 2814.5; DB 2; Length 854;
Best Local Similarity 82.9%; Pred. No. 7.8e-224;
Matches 540; Conservative 34; Mismatches 56; Indels 21; Gaps 9;
Qy 3 LWTVYVYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTENF 62
Db 34 LWTVYVYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTENF 93
Qy 63 NMWKNMVEQMHEDIISLWDSQKPCVKLTPLCVTLNCTDLNTNTNTTSLSIIVVWEQ 122
Db 94 NMWKNMVEQMHEDIISLWDSQKPCVKLTPLCVTLNCTDLNTNTNTSSGRIME- 150
Qy 123 RGKEMRNCFSNITTSIRDKVOREVALFYKLDVPEIDNKNNTNTKYLINCNMTSVITQ 182
Db 151 --KGEIKNCFSNITTSIRDKVOREVALFYKLDIVPID-----NTSYRLISCNMTSVITQ 201
Qy 183 ACPKVSPEPIPIHYCTPTGFAILLKCNKDKFNGTGTCTVSTVQCTHGRPVVSTOLLING 242
Db 202 ACPKVSPEPIPIHYCAPAGFAILKCNKNTFNGTGTCTVSTVQCTHGRPVVSTOLLING 261

Qy 243 SLAEEDVIRSNFTNNAKTIIVQLNVSVINCTRPNNHTRK--RVTLGPGRVWVTTGEBI 300
Db 262 SLAEEDVIRSNFTNNAKTIIVQLNVSVINCTRPNNHTRKSIIRIQPGRAFVTIGKI 321
Qy 301 LGNIROAHCHNISRAQWNTLQOIATTLREOFG-NKTIAPNOSGGDPPIVMSHFNCGGEF 359
Db 322 -GNMROAHCHNISRAQWNTLQOIATTLREOFGNNTIIFKOSGGDPPIVTHSFNCGGEF 380
Qy 360 FYCNSTOLFNSAWNTSNGTWSVTRKQKDTG-DIITLPCRILQIINRWQVVGKAMALPI 418
Db 381 FYCNSTOLFNSW---FNSWSTEGSNNTGSDTITLPCRILQIINRWQVVGKAMALPI 437
Qy 419 KGLIRCSNITGLLLTRDGGGNGOTTEIFRPGGDMRDNRSELYKYKVVKIEPLGVAPT 478
Db 438 SGOIRCSNITGLLLTRDGGGNNNGSEIFRPGGDMRDNRSELYKYKVVKIEPLGVAPT 497
Qy 479 KAKRVVOREKRAVGMFLGFLGAAGSTMGATSMALTVOARQLLSGI VQQNNLLRA 538
Db 498 KAKRVVOREKRAVG-IGALFLGFLGAAGSTMGCTSMTLTVOARQLLSDI VQQNNLLRA 556
Qy 539 IKAQOHLQLTWGILKQIARILAVERYLKQOQLLGFWGC SGKLICTTAVPWNASWSNKT 598
Db 557 IEAQOHLQLTWGILKQIARILAVERYLKQOQLLGFWGC SGKLICTTAVPWNASWSNKS 616
Qy 599 LDQIWNNTMWEWDREINNYTHLYTLIESONQOEKQOQLLQDKWASL 649
Db 617 LEQIWNNTMWEWDREINNYTHLYTLIESONQOEKQOQLLQDKWASL 667

RESULT 14

US-09-718-096-23
; Sequence 23, Application US/09718096
; Patent No. 6589763
; GENERAL INFORMATION:
; APPLICANT: Von Laer, Meike-Dorothee
; TITLE OF INVENTION: RETROVIRAL HYBRID VECTORS PSEUDOTYPED WITH LCMV
; FILE REFERENCE: 35-195
; CURRENT APPLICATION NUMBER: US/09/718,096
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: DE 19856463.5
; PRIOR FILING DATE: 1998-11-26
; PRIOR APPLICATION NUMBER: EP 99250415.9
; PRIOR FILING DATE: 1999-11-25
; PRIOR APPLICATION NUMBER: US 09/309,572
; PRIOR FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 854
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: envelope polyprotein
US-09-718-096-23

Query Match 81.0%; Score 2814.5; DB 2; Length 854;
Best Local Similarity 82.9%; Pred. No. 7.8e-224;
Matches 540; Conservative 34; Mismatches 56; Indels 21; Gaps 9;
Qy 3 LWTVYVYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTENF 62
Db 34 LWTVYVYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTENF 93
Qy 63 NMWKNMVEQMHEDIISLWDSQKPCVKLTPLCVTLNCTDLNTNTNTTSLSIIVVWEQ 122
Db 94 NMWKNMVEQMHEDIISLWDSQKPCVKLTPLCVTLNCTDLNTNTNTSSGRIME- 150
Qy 123 RGKEMRNCFSNITTSIRDKVOREVALFYKLDVPEIDNKNNTNTKYLINCNMTSVITQ 182
Db 151 --KGEIKNCFSNITTSIRDKVOREVALFYKLDIVPID-----NTSYRLISCNMTSVITQ 201
Qy 183 ACPKVSPEPIPIHYCTPTGFAILLKCNKDKFNGTGTCTVSTVQCTHGRPVVSTOLLING 242

Db 202 ACPKVSPEPIHYCAPAGFAILKCNKNTFNGTCTNVTSTVQCTHGRVPVSTQLLLNG 261
Qy 243 SLAEVVIRSENFTNNAKTIIVOLNVSEINCTRPNNHTRK--RVTLGPRVYVYTTGEI 300
Db 262 SLAEEDVIRSANFTDNAKTIIVOLNTSVEINCTRPNNHTRKSIIRIQRGFGRAFVTIGKI 321
Qy 301 LGNIRQAHCNISRAQWNTTLOQIATTLREQFG-NKTIAPNQSSGGDPEIWMHSPNCGGEF 359
Db 322 -GNMROAHCNISRAKWNTLQIASKLREQFGNNTIIFKQSSGGDPEIIVTHSFNCGGEF 380
Qy 360 FYCNSTQLFNSAMVNTSNGTWSVTRKQKDTG-DIITLPCRILKQILNRQVVGKAWALPI 418
Db 381 FYCNSTQLFNSW---FNSTWSTEGSNNTSGSDTITLPCRILKQILNRQVVGKAWAPPI 437
Qy 419 KGLRCSNNTIGLLTRDGGGENTTEIFRPGGDMRDNRSSELYKYKVKIPLGVAPT 478
Db 438 SGQIRCSNNTIGLLTRDGGNNNGSEIFRPGGDMRDNRSSELYKYKVKIPLGVAPT 497
Qy 479 KAKERVVQREKRAVGMFLGAMFLGFLGAAGSTMGATSMALTVOARQLLSGIVQQNNLLRA 538
Db 498 KAKERVVQREKRAVG-IGALFLGFLGAAGSTMGCTSWTLTVQARQLLSGIVQQNNLLRA 556
Qy 539 IKAQOHLQLTVMGIKQOLARILAVERYLKDQQLLGPWCGSGKLICTTAVPMNASMKNKT 598
Db 557 IEAQOHLQLTVMGIKQOLARILAVERYLKDQQLLGIWCGSGKLICTTAVPMNASMKNKS 616
Qy 599 LDQIWNMTWMDREIDNYTHLYTLIESONQOEKNOQELLDKQWASL 649
Db 617 LEQIWNMTWMDREINNYTSLIHSLEESQOEKNEQELLELDKQWASL 667

RESULT 15

US-08-788-815-7
; Sequence 7, Application US/08788815
; Patent No. 5846546
; GENERAL INFORMATION:
; APPLICANT: St. Jude Children's Research Hospital
; APPLICANT: 332 No. 5846546th Lauderdale
; APPLICANT: PO Box 318
; APPLICANT: Memphis, TN 38101-0318
; APPLICANT: United States of America
; APPLICANT: Coleclough, Christopher
; APPLICANT: Owens, Randall J.
; APPLICANT: Slobod, Karen
; TITLE OF INVENTION: PREPARATION AND USE OF VIRAL VECTORS FOR
; TITLE OF INVENTION: MIXED ENVELOPE PROTEIN VACCINES AGAINST HUMAN
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KLAUBER & JACKSON
; STREET: 411 HACKENSACK AVENUE
; CITY: HACKENSACK
; STATE: NJ
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,815
; FILING DATE: Herewith
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul F. Fehlner
; REGISTRATION NUMBER: 35,135
; REFERENCE/DOCKET NUMBER: 1340-1-011CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 880 amino acids
; TYPE: amino acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: protein
; US-08-788-815-7

Query Match 81.0%; Score 2814; DB 1; Length 880;
Best Local Similarity 82.1%; Pred. No. 8 9e-224;
Matches 540; Conservative 39; Mismatches 61; Indels 18; Gaps 9;

Qy 3 LWTVVYVGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTENF 62
Db 43 LWTVVYVGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTENF 102
Qy 63 NMKKNMVQOMHEDIISLWDQSLKPCVKLTPLCVTLNCTDL--NTNNTNTTSLSIIVW 120
Db 103 NMKKNMVQOMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLKNDTNTNNVTSS---W 158
Qy 121 EQR--GKGEWRNCSFNITTSIRDKVQREYALFYKLDVEPID--DNKNTNTNTKYRLN 176
Db 159 GRNIMEGEIKNCSFNISTISIRKVOKEYAFFYKLDIIPIDKGNDSNDTTSYKFTTSCN 218
Qy 177 TSVITQACPKVSEPIPIHYCTPTGFPALLKCNDDKFNKGTPCTNVTSTVQCTHGRVPVST 236
Db 219 TSVITQACPKVSEPIPIHYCAPAGFAILKCNKNTFNGTCTNVTSTVQCTHGRVPVST 278
Qy 237 QLLNGSLAEVEVIRSENFTNNAKTIIVQLNVSEINCTRPNNHTRK--RVTLGPRVW 294
Db 279 QLLNGSLAEVEVIRSANFTDNAKTIIVQLNQSVBEINCTRPNNHTRKSIIRIQRGFGRAF 338
Qy 295 YTTGTEILGNIRQAHCNISRAQWNTTLOQIATTLREQFG-NKTIAPNQSSGGDPEIWMHSP 353
Db 339 VTIGKILGNMROAHCNISRAKWNTLQIASKLREQFGNNTIIFKQSSGGDPEIIVTHSF 398
Qy 354 NCGGEFFYCNSTQLFNSAMVNTSNGTWSVTRKQKDTG-DIITLPCRILKQILNRQVVGKA 412
Db 399 NCGGEFFYCNSTQLFNSW---FNSTWSTEGSNNTSGSDTITLPCRILKQILNRQVVGKA 455
Qy 413 MYALPIKGLIRCSNNTIGLLTRDGG-GENOTTEIFRPGGDMRDNRSSELYKYKVKIE 471
Db 456 MYAPPISGGIIRCSNNTIGLLTRDGGANENNESEIFRPGGDMRDNRSSELYKYKVKIE 515
Qy 472 PLGVAPTAKRRVVQREKRAVGMFLGAMFLGFLGAAGSTMGATSMALTVOARQLLSGIVQ 531
Db 516 PLGVAPTAKRRVVQREKRAVGEIGALFLGFLGAAGSTMGASMTLTVQARQLLSGIVQ 575
Qy 532 QNNLLRAIKAQOHLQLTVMGIKQOLARILAVERYLKDQQLLGPWCGSGKLICTTAVPMN 591
Db 576 QNNLLRAIEAQOHLQLTVMGIKQOLARILAVERYLKDQQLLGIWCGSGKLICTTAVPMN 635
Qy 592 ASWSNKTLDQIWNMTWMDREIDNYTHLYTLIESONQOEKNOQELLDKQWASL 649
Db 636 ASWSNKSLEQIWNMTWMDREINNYTSLIHSLEESQOEKNEQELLELDKQWASL 693

Search completed: March 7, 2006, 17:52:51
Job time : 69.9631 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 7, 2006, 17:51:52 ; Search time 211.547 Seconds
(without alignments)
1281.847 Million cell updates/sec

Title: US-09-938-406-1_COPY_33_681

Perfect score: 3474

Sequence: 1 ANLWTVYGVVWKEATTT.....QNQEKNOQELLQDKWASL 649

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3474	100.0	868	3	US-09-938-406-1
2	2987	86.0	862	5	US-10-780-507-51
3	2977.5	85.7	883	4	US-10-441-926-2
4	2977.5	85.7	883	4	US-10-441-949-2
5	2977.5	85.7	883	5	US-10-780-507-2
6	2977.5	85.7	883	5	US-10-780-507-121
7	2949	84.9	862	5	US-10-780-507-50
8	2896.5	83.4	852	4	US-10-093-953A-29
9	2883.5	83.0	842	4	US-10-190-435-2
10	2883.5	83.0	842	4	US-10-241-009-2
11	2883.5	83.0	842	4	US-10-190-434B-2
12	2883.5	83.0	842	4	US-10-190-305A-2
13	2883.5	83.0	842	5	US-10-976-619-2
14	2883.5	83.0	847	3	US-09-476-242-2
15	2852	82.1	850	3	US-09-966-931-28
16	2852	82.1	850	4	US-10-459-121-28
17	2827.5	81.4	643	4	US-10-032-162-13
18	2827.5	81.4	643	5	US-10-780-993-13
19	2809.5	80.9	856	3	US-09-476-242-1
20	2809.5	80.9	856	5	US-10-891-825-19
21	2809.5	80.9	857	3	US-09-966-931-30
22	2809.5	80.9	857	4	US-10-459-121-30
23	2807	80.8	848	5	US-10-844-658-1
24	2806.5	80.8	863	5	US-10-634-165-11
25	2795.5	80.5	856	4	US-10-196-515-11
26	2795.5	80.5	856	6	US-11-048-554-11
27	2795	80.5	861	4	US-10-026-741-103

28	2790.5	80.3	643	4	US-10-375-657-7	Sequence 7, Appli
29	2789.5	80.3	667	5	US-10-506-651-4	Sequence 4, Appli
30	2789.5	80.3	853	5	US-10-506-651-2	Sequence 2, Appli
31	2781	80.1	665	3	US-09-966-931-32	Sequence 32, Appli
32	2781	80.1	665	4	US-10-459-121-32	Sequence 32, Appli
33	2771.5	79.8	856	5	US-10-844-658-5	Sequence 5, Appli
34	2757	79.4	726	4	US-10-196-515-3	Sequence 3, Appli
35	2757	79.4	726	6	US-11-048-554-3	Sequence 3, Appli
36	2755	79.3	759	4	US-10-196-515-12	Sequence 12, Appli
37	2755	79.3	759	6	US-11-048-554-12	Sequence 12, Appli
38	2736.5	78.8	849	4	US-10-325-468-15	Sequence 15, Appli
39	2736.5	78.8	855	4	US-10-325-468-25	Sequence 25, Appli
40	2729.5	78.6	849	4	US-10-325-468-32	Sequence 32, Appli
41	2728.5	78.5	619	3	US-09-891-609-4	Sequence 4, Appli
42	2728.5	78.5	646	3	US-09-891-609-2	Sequence 2, Appli
43	2728.5	78.5	849	4	US-10-325-468-29	Sequence 29, Appli
44	2720.5	78.3	625	4	US-10-032-162-17	Sequence 17, Appli
45	2720.5	78.3	625	5	US-10-780-993-17	Sequence 17, Appli

ALIGNMENTS

RESULT 1

US-09-938-406-1
; Sequence 1, Application US/09938406
; Patent No. US20020155120A1
; GENERAL INFORMATION:
; APPLICANT: Lowell, George
; APPLICANT: Vancott, Thomas
; APPLICANT: Birx, Deborah
; TITLE OF INVENTION: PROTEIN AND PEPTIDE VACCINES FOR
; TITLE OF INVENTION: INDUCING MUCOSAL IMMUNITY
; FILE REFERENCE: 40646-20002.10
; CURRENT APPLICATION NUMBER: US/09/938,406
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/214,701
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: PCT/US 97/12253
; PRIOR FILING DATE: 1997-07-10
; PRIOR APPLICATION NUMBER: US 60/021,687
; PRIOR FILING DATE: 1996-07-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 868
; TYPE: PRT
; ORGANISM: Virus HIV-1
US-09-938-406-1

Query Match						100.0%; Score 3474; DB 3; Length 868;
Best Local Similarity						100.0%; Pred. No. 2.8e-266;
Matches						649; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	ANLWTVYGVVWKEATTTFCASAKAYDTAHNWNWATHACVPTNPQEVLENVTE	60			
Db	33	ANLWTVYGVVWKEATTTFCASAKAYDTAHNWNWATHACVPTNPQEVLENVTE	92			
Qy	61	NFNWKNMNVQEMHEDIISLWDSQKPCVKLTPLCVTLNCTDLNNTNTTTELSIIVW	120			
Db	93	NFNWKNMNVQEMHEDIISLWDSQKPCVKLTPLCVTLNCTDLNNTNTTTELSIIVW	152			
Qy	121	EORGKGMNCSNITTSIRDKVQREYALFKLDVEPIDDKNTNTNTRKRLINCNTSVI	180			
Db	153	EORGKGMNCSNITTSIRDKVQREYALFKLDVEPIDDKNTNTNTRKRLINCNTSVI	212			
Qy	181	TQACPKVSFPIPIHYCTPTGFALLKCNKKFKGTGCTNVSTVQCTHGRPVVSTQLLL	240			
Db	213	TQACPKVSFPIPIHYCTPTGFALLKCNKKFKGTGCTNVSTVQCTHGRPVVSTQLLL	272			
Qy	241	NGSLAEVEVIRSENFNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGEI	300			
Db	273	NGSLAEVEVIRSENFNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGEI	332			

QY	301	LGNIROAHCNISRAQWNNTLQOIATTLREQFGNKTIAFNQSSGDDPEIVMHSFNCGEFF	360
Db	333	LGNIROAHCNISRAQWNNTLQOIATTLREQFGNKTIAFNQSSGDDPEIVMHSFNCGEFF	392
QY	361	YCNSTQLFNSAWNTSNGTWSVTRKQKDTGDIITLPCRIOIINRWQVVGKAMYPKIG	420
Db	393	YCNSTQLFNSAWNTSNGTWSVTRKQKDTGDIITLPCRIOIINRWQVVGKAMYPKIG	452
QY	421	LIRCSSNITGLLTRDGGGENTTEIPRPGGDMRDNRSELYKYKVKIEPLGVAPTKA	480
Db	453	LIRCSSNITGLLTRDGGGENTTEIPRPGGDMRDNRSELYKYKVKIEPLGVAPTKA	512
QY	481	KRRVQREKRAVGMGLGFLGAAGSTMGATSMALTVOARQLLSGIVQQNNLLRAIK	540
Db	513	KRRVQREKRAVGMGLGFLGAAGSTMGATSMALTVOARQLLSGIVQQNNLLRAIK	572
QY	541	AQOHLQLTVMGIKOLOARILAVERYLKDQQLLGFWGCSSGLICTTAVPWNASWSNKTLD	600
Db	573	AQOHLQLTVMGIKOLOARILAVERYLKDQQLLGFWGCSSGLICTTAVPWNASWSNKTLD	632
QY	601	QIWNNTMTWMDREIDNTHLYITLIEESQOQEKNOQELLQLDKWASL	649
Db	633	QIWNNTMTWMDREIDNTHLYITLIEESQOQEKNOQELLQLDKWASL	681
RESULT 2			
US-10-780-507-51			
; Sequence 51, Application US/10780507			
; Publication No. US20050137387A1			
; GENERAL INFORMATION:			
; APPLICANT: MULLINS, James I.			
; APPLICANT: RODRIGO, Allen G.			
; APPLICANT: LEARN, Gerald H.			
; APPLICANT: LI, Fusheng			
; APPLICANT: NICKLE, David C.			
; APPLICANT: JENSEN, Mark A.			
; TITLE OF INVENTION: ANCESTRAL AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPO			
; FILE REFERENCE: 16336-001320US			
; CURRENT APPLICATION NUMBER: US/10/780,507			
; CURRENT FILING DATE: 2004-02-17			
; PRIOR APPLICATION NUMBER: US 10/204,204			
; PRIOR FILING DATE: 2001-02-16			
; PRIOR APPLICATION NUMBER: PCT/US01/05288			
; PRIOR FILING DATE: 2001-02-16			
; PRIOR APPLICATION NUMBER: US 60/183,659			
; PRIOR FILING DATE: 2000-02-18			
; PRIOR APPLICATION NUMBER: US 60/447,586			
; PRIOR FILING DATE: 2003-02-14			
; NUMBER OF SEQ ID NOS: 125			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 51			
; LENGTH: 862			
; TYPE: PRT			
; ORGANISM: Artificial sequence			
; FEATURE:			
; OTHER INFORMATION: Least squares and minimum of means center of tree reconstruction			
; OTHER INFORMATION: of clade B gp 160 protein sequence			
US-10-780-507-51			
Query Match 86.0%; Score 2987; DB 5; Length 862;			
Best Local Similarity 86.6%; Pred. No. 1.1e-227;			
Matches 563; Conservative 31; Mismatches 46; Indels 10; Gaps 6;			
QY	3	LWTVVYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPPOEVLENTENF	62
Db	33	LWTVVYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPPOEVLENTENF	92
QY	63	NMKNMNVQEMHEDIISLWDSKPCVKLTPLCVTLNCTDLNNTNTTTELIIIVVWQ	122
Db	93	NMKNMNVQEMHEDIISLWDSKPCVKLTPLCVTLNCTDLN-KNATNTSSS-----GEM	147
QY	123	RKGEMRNCNFTTTSIRDKVQREYALFYKLDVEIPDDNKNTNTNTKYRLINCNTSVITQ	182

Db	148	MEKGEIKNCNFTTTSIRDKVQREYALFYKLDVVPIDNDNNTNTTTSYRLISCNTSVITQ	207
QY	183	ACPKVSEFPIPHYCTPTGCFALLKNDKKFNGTGPCTNVSTVOCTHGIRPVVSTQLLNG	242
Db	208	ACPKVSEFPIPHYCAPAGFAILLKNDKKFNGTGPCTNVSTVOCTHGIRPVVSTQLLNG	267
QY	243	SLAESEVWIRSENFTNNAKTIIVQLNVSEINCTRENHTRKRVTLGPRVWYTTGEILG	302
Db	268	SLAESEVWIRSDNFTNAKTIIVQLNVSEINCTRENHTRKSIHIGPGRFVTTGEILG	327
QY	303	NIRQAHCNISRAQWNNTLOOIATTLREQFG-NKTIAFNOSGGDDPEIVMHSFNCGEFFY	361
Db	328	DIRQAHCNISRAQWNNTLQIIVKLLREQFGNKTIVFNQSSGDDPEIVMHSFNCGEFFY	387
QY	362	CNSTOLFNSAWNTSNGTWSVTRKQKDT-GDIITLPCRIOIINRWQVVGKAMYPKIG	420
Db	388	CNSTOLFNSWTNGT--WTWNTTEGSDNTEGDTITLPCRIOIINRWQVVGKAMYPKIG	445
QY	421	LIRCSSNITGLLTRDGGGEN-OTTETPRPGGDMRDNRSELYKYKVKIEPLGVAPT	479
Db	446	QIRCSSNITGLLTRDGGGNNTNETEIPRPGGDMRDNRSELYKYKVKIEPLGVAPT	505
QY	480	KRRVQREKRAVGMGLGFLGAAGSTMGATSMALTVOARQLLSGIVQQNNLLRAI	539
Db	506	KRRVQREKRAVGITGAVFLGFLGAAGSTMGAASTMTLTVQARQLLSGIVQQNNLLRAI	565
QY	540	KAOHLQLTVMGIKOLOARILAVERYLKDQQLLGFWGCSSGLICTTAVPWNASWSNKT	599
Db	566	EAOHLQLTVMGIKOLOARILAVERYLKDQQLLGFWGCSSGLICTTAVPWNASWSNKS	625
QY	600	DOIWNNTMTWMDREIDNTHLYITLIEESQOQEKNOQELLQLDKWASL	649
Db	626	DEIWNNTMTWMDREIDNTHLYITLIEESQOQEKNEQELLELDKWASL	675
RESULT 3			
US-10-441-926-2			
; Sequence 2, Application US/10441926			
; Publication No. US20040115621A1			
; GENERAL INFORMATION:			
; APPLICANT: Rodrigo, Allen			
; APPLICANT: Ross, Howard A.			
; APPLICANT: Mullins, James I.			
; TITLE OF INVENTION: ANCESTRAL VIRUSES AND VACCINES			
; FILE REFERENCE: 08987-011001			
; CURRENT APPLICATION NUMBER: US/10/441,926			
; CURRENT FILING DATE: 2003-05-19			
; PRIOR APPLICATION NUMBER: PCT/US01/05288			
; PRIOR FILING DATE: 2001-02-18			
; PRIOR APPLICATION NUMBER: US 60/183,659			
; PRIOR FILING DATE: 2000-02-18			
; NUMBER OF SEQ ID NOS: 42			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 2			
; LENGTH: 883			
; TYPE: PRT			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Artificially generated peptide			
US-10-441-926-2			
Query Match 85.7%; Score 2977.5; DB 4; Length 883;			
Best Local Similarity 84.7%; Pred. No. 6.5e-227;			
Matches 564; Conservative 27; Mismatches 54; Indels 21; Gaps 6;			
QY	3	LWTVVYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPPOEVLENTENF	62
Db	33	LWTVVYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPPOEVLENTENF	92
QY	63	NMKNMNVQEMHEDIISLWDSKPCVKLTPLCVTLNCTDLNNTTTELIIIVVWQ	122
Db	93	NMKNMNVQEMHEDIISLWDSKPCVKLTPLCVTLNCTDLNRTATNTNTSSATNTTTS	152


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; SEQ ID NO 2
; LENGTH: 883
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ancestral HIV-1 group M, subtype B, env sequence
US-10-780-507-2

Query Match      85.7%; Score 2977.5; DB 5; Length 883;
Best Local Similarity 84.7%; Pred. No. 6.5e-227;
Matches 564; Conservative 27; Mismatches 54; Indels 21; Gaps 6;

Qy 3 LWTVVYGVVPWKAEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 62
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 33 LWTVVYGVVPWKAEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 92
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 63 NMKNMNVQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNNTNTTSSATTNTS 122
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 93 NMKNMNVQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNNTNTTSSATTNTS 152
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 123 RG-----KGMNRCNFNITTSIRDKVQREYALFYKLDVEPID-DNKNTNTTKYRLIN 174
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 153 SGGTMEGEKEIKNCSEFNVTTSIRDKQKEYALFYKLDVVPIDNNDNNNTNNTSYRLIN 212
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 175 CNTSVITQACPKVSFEPIPIHYCTPTGFAILLKNDKFKNGTGPCTNVSTVQCTHGIRPVV 234
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 213 CNTSVITQACPKVSFEPIPIHYCTPAGFAILLKNDKFKNGTGPCTNVSTVQCTHGIRPVV 272
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 235 STOLLNGSLAEEVIRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPGVW 294
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 273 STOLLNGSLAEEVIRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPGVW 332
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 295 YTTGEILGNIRQAHCNISRAQWNTLQIATTLREOFGNK--TIAFNQSSGGDPEIVMHS 352
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 333 YATGKIIGDIRQAHCNLSRAKWNNTLKQIVTKLREQFGNNKTTIVFNQSSGGDPEIVMHS 392
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 353 FNCGGEFFYCNSTOLFNSAWNTSNGTWSVTRKQK-----DTGDIITLPCRKQIINRWQ 407
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 393 FNCGGEFFYCNSTOLFNSAWNTSNGTWSVTRKQK-----DTGDIITLPCRKQIINRWQ 450
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 408 VVGKAMYPALPKGLIRCSSNITGLLITRDGGGNGT-----TEIFRPGGDMRDNRSELY 463
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 451 EVGKAMYPALPKGLIRCSSNITGLLITRDGGGNGT-----TEIFRPGGDMRDNRSELY 510
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 464 KYKVKIEPLGVAPTAKRVVQREKAVGMGLGAMFLGFLGAGSTMGATSMALTVOARQ 523
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 511 KYKVKIEPLGVAPTAKRVVQREKAVGMGLGAMFLGFLGAGSTMGATSMALTVOARQ 570
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 524 LLSGIVQOQNLLRAIKAOQHLLQLTWVGIKQIARILAVERYLKDQQLGFGWCSGKLI 583
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 571 LLSGIVQOQNLLRAIKAOQHLLQLTWVGIKQIARILAVERYLKDQQLGFGWCSGKLI 630
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 584 CTTAVPWNASWNTLDQIWNNTMWEWDREIDNYTHLYTLIEESQNOQEKQOELLQ 643
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 631 CTTAVPWNASWNTLDQIWNNTMWEWDREIDNYTHLYTLIEESQNOQEKQOELLQ 690
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 644 DKWASL 649
Db | | | | |
Qy 691 DKWASL 696
Db | | | | |

RESULT 6
US-10-780-507-121
; Sequence 121, Application US/10780507
; Publication No. US20050137387A1
; GENERAL INFORMATION:
; APPLICANT: MULLINS, James I.
; APPLICANT: RODRIGO, Allen G.
; APPLICANT: LEARN, Gerald H.
; APPLICANT: LI, Fusheng
; APPLICANT: NICKLE, David C.
; APPLICANT: JENSEN, Mark A.
; TITLE OF INVENTION: ANCESTRAL AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPO

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; FILE REFERENCE: 16336-001320US
; CURRENT APPLICATION NUMBER: US/10/780,507
; PRIOR FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US 10/204,204
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: PCT/US01/05288
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 60/183,659
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/447,586
; PRIOR FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 121
; LENGTH: 883
; TYPE: PR1
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Deduced ancestor env protein sequence
US-10-780-507-121

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Query Match      85.7%; Score 2977.5; DB 5; Length 883;
Best Local Similarity 84.7%; Pred. No. 6.5e-227;
Matches 564; Conservative 27; Mismatches 54; Indels 21; Gaps 6;

Qy 3 LWTVVYGVVPWKAEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 62
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 33 LWTVVYGVVPWKAEATTLFCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 92
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 63 NMKNMNVQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNNTNTTSSATTNTS 122
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 93 NMKNMNVQMHEDIISLWDQSLKPCVKLTPLCVTLNCTDLNNTNTTSSATTNTS 152
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 123 RG-----KGMNRCNFNITTSIRDKVQREYALFYKLDVEPID-DNKNTNTTKYRLIN 174
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 153 SGGTMEGEKEIKNCSEFNVTTSIRDKQKEYALFYKLDVVPIDNNDNNNTNNTSYRLIN 212
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 175 CNTSVITQACPKVSFEPIPIHYCTPTGFAILLKNDKFKNGTGPCTNVSTVQCTHGIRPVV 234
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 213 CNTSVITQACPKVSFEPIPIHYCTPAGFAILLKNDKFKNGTGPCTNVSTVQCTHGIRPVV 272
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 235 STOLLNGSLAEEVIRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPGVW 294
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 273 STOLLNGSLAEEVIRSENFNTNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPGVW 332
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 295 YTTGEILGNIRQAHCNISRAQWNTLQIATTLREOFGNK--TIAFNQSSGGDPEIVMHS 352
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 333 YATGKIIGDIRQAHCNLSRAKWNNTLKQIVTKLREQFGNNKTTIVFNQSSGGDPEIVMHS 392
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 353 FNCGGEFFYCNSTOLFNSAWNTSNGTWSVTRKQK-----DTGDIITLPCRKQIINRWQ 407
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 393 FNCGGEFFYCNSTOLFNSAWNTSNGTWSVTRKQK-----DTGDIITLPCRKQIINRWQ 450
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 408 VVGKAMYPALPKGLIRCSSNITGLLITRDGGGNGT-----TEIFRPGGDMRDNRSELY 463
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 451 EVGKAMYPALPKGLIRCSSNITGLLITRDGGGNGT-----TEIFRPGGDMRDNRSELY 510
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 464 KYKVKIEPLGVAPTAKRVVQREKAVGMGLGAMFLGFLGAGSTMGATSMALTVOARQ 523
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 511 KYKVKIEPLGVAPTAKRVVQREKAVGMGLGAMFLGFLGAGSTMGATSMALTVOARQ 570
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 524 LLSGIVQOQNLLRAIKAOQHLLQLTWVGIKQIARILAVERYLKDQQLGFGWCSGKLI 583
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 571 LLSGIVQOQNLLRAIKAOQHLLQLTWVGIKQIARILAVERYLKDQQLGFGWCSGKLI 630
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 584 CTTAVPWNASWNTLDQIWNNTMWEWDREIDNYTHLYTLIEESQNOQEKQOELLQ 643
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 631 CTTAVPWNASWNTLDQIWNNTMWEWDREIDNYTHLYTLIEESQNOQEKQOELLQ 690
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 644 DKWASL 649
Db | | | | |
Qy 691 DKWASL 696
Db | | | | |

```

RESULT 7
US-10-780-507-50
; Sequence 50, Application US/10780507
; Publication No. US2005013787A1
; GENERAL INFORMATION:
; APPLICANT: MULLINS, James I.
; APPLICANT: RODRIGO, Allen G.
; APPLICANT: LEARN, Gerald H.
; APPLICANT: Li, Fusheng
; APPLICANT: JENSEN, Mark A.
; TITLE OF INVENTION: ANCESTRAL AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPO
; FILE REFERENCE: 16336-001320US
; CURRENT APPLICATION NUMBER: US/10/780,507
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US 10/204,204
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: PCT/US01/05288
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 60/183,659
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/447,586
; PRIOR FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 50
; LENGTH: 862
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Most recent common ancestor reconstruction of clade B gp 160 prot
; OTHER INFORMATION: ein sequence
US-10-780-507-50

Query Match 84.9%; Score 2949; DB 5; Length 862;
Best Local Similarity 85.6%; Pred. No. 1.1e-224; Mismatches 52; Indels 10; Gaps 6;
Matches 557; Conservative 32

Qy 2 NLWTVVYGVVPMKEATTTLCASDAKAYDEAHNVWATHACVPTNPQEWLVNVTEN 61
Db 32 NLWTVVYGVVPMKEATTTLCASDAKAYDEVHNVWATHACVPTNPQEWLVNVTEN 91

Qy 62 FNMKNVNVQMHEDIISLWDSQSLKPCVKLPCLVTLNCTDLNNTNTTNTTSLIIVWE 121
Db 92 FNMKNVNVQMHEDIISLWDSQSLKPCVKLPCLVTLNCTDLNNTNTNSSS---GG 146

Qy 122 QRGKGMKNCNFNTTISRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCNSTVIT 181
Db 147 TMRGEMKNCNFNTTISRDKVQREYALFYKLDVVPIDNNDNNNTNTYRLINCNSTVIT 206

Qy 182 QACPKVSFPIPIHYCTPTGTFALLKCNDDKFKNGTGPCTNVSTVCTGIRPVWSTQLLN 241
Db 207 QACPKVSFPIPIHYCTPTGTFALLKCNDDKFKNGTGPCKNVSTVCTGIRPVWSTQLLN 266

Qy 242 GSIAEEVVRISNFTNNAKTIIVQLNVSVVEINCTRPNNHTRKRVTLGPGRWYTTGAIL 301
Db 267 GSIAEEVVRISNFTNNAKTIIVQLNVSVVEINCTRPNNHTRKRVTLGPGRWYTTGAIL 326

Qy 302 GNIQAHCNISRAOWNNTLOIATILRBOFG-NKTIAPNQSGGDPPEIVMHSFNCGGEFF 360
Db 327 GDIRQAHCNISRAOWNNTLOIATILRBOFG-NKTIAPNQSGGDPPEIVMHSFNCGGEFF 386

Qy 361 YCNSQLPNSAWNTVSTGWSVTRKQKDTGDIITLPCRIKOLINRWQVGVKAMVALPLKG 420
Db 387 YCNSQLPNSAWNTVSTGWSVTRKQKDTGDIITLPCRIKOLINRWQVGVKAMVALPLKG 445

Qy 421 LIRCSSNITGLLLTRDGGENQOT--TEIFRPGGDMRDNRWSELYKYKVKVIEPLGVAPT 478
Db 446 QIKCSSNITGLLLTRDGGENQOT--TEIFRPGGDMRDNRWSELYKYKVKVIEPLGVAPT 504

Qy 479 KAKRRVVQREKRAVGMGLGAMFLGFLGAAAGSTGMAATLTVQARQLLSGIVQQNNLLRA 538
Db 504 KAKRRVVQREKRAVGMGLGAMFLGFLGAAAGSTGMAATLTVQARQLLSGIVQQNNLLRA 564

Db 505 KAKRRVVQREKRAVGMGLGAMFLGFLGAAAGSTGMAATLTVQARQLLSGIVQQNNLLRA 564
Qy 539 IKAQHLLQLTVMGIKOQARILAVERYLKDQQLLGFWGCCKLICCTTAVPWNASWSNKT 598
Db 565 IEAQHLLQLTVMGIKOQARILAVERYLKDQQLLGFWGCCKLICCTTAVPWNASWSNKS 624
Qy 599 LDQIWNNTWMDREIDNTYTHLYTLIESQNOEKNOQELLQDLKQWASL 649
Db 625 LDKIWNNTWMDREIDNTYTHLYTLIESQNOEKNOQELLQDLKQWASL 675

RESULT 8
US-10-093-953A-29
; Sequence 29, Application US/10093953A
; Publication No. US20040105871A1
; GENERAL INFORMATION:
; APPLICANT: Robinson, Harriet L.
; APPLICANT: Smith, James M.
; APPLICANT: Hua, Jian
; APPLICANT: Moss, Bernard
; APPLICANT: Amara, Rama
; APPLICANT: Wyatt, Linda
; APPLICANT: Earl, Patricia
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENERATING
; FILE REFERENCE: 12804-005002
; CURRENT APPLICATION NUMBER: US/10/093,953A
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US 60/186,364
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/251,083
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/799,675
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: PCT/US01/06795
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/324,845
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/325,004
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 852
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: protein encoded by construct of vaccine vector
; OTHER INFORMATION: pGA2 and insert JS2 expressing clade HIV-1 VL
US-10-093-953A-29

Query Match 83.4%; Score 2896.5; DB 4; Length 852;
Best Local Similarity 83.6%; Pred. No. 1.6e-220; Mismatches 40; Indels 19; Gaps 6;
Matches 544; Conservative 40

Qy 2 NLWTVVYGVVPMKEATTTLCASDAKAYDEAHNVWATHACVPTNPQEWLVNVTEN 61
Db 32 NLWTVVYGVVPMKEATTTLCASDAKAYDEVHNVWATHACVPTNPQEWLVNVTEN 91

Qy 62 FNMKNVNVQMHEDIISLWDSQSLKPCVKLPCLVTLNCTDLNNTNTTNTTSLIIVW 120
Db 92 FNMKNVNVQMHEDIISLWDSQSLKPCVKLPCLVTLNCTDLNNTNTNINSS- 144

Qy 121 EQRGKGMKNCNFNTTISRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCNSTVI 180
Db 145 --GMRGKGMKNCNFNTTISRDKVQREYALFYKLDVEPIDDKNTNTNTKYRLINCNSTVI 197

Qy 181 TOACPKVSFPIPIHYCTPTGTFALLKCNDDKFKNGTGPCTNVSTVCTGIRPVWSTQLLN 240
Db 198 TOACPKVSFPIPIHYCTPTGTFALLKCNDDKFKNGTGPCKNVSTVCTGIRPVWSTQLLN 257

Qy 241 NGSIAEEVVRISNFTNNAKTIIVQLNVSVVEINCTRPNNHTRKRVTLGPGRWYTTGAIL 300
Db 257 NGSIAEEVVRISNFTNNAKTIIVQLNVSVVEINCTRPNNHTRKRVTLGPGRWYTTGAIL 300

```

Db 258 NGLAEVEVIRSNFTDNNKIIIVQLKESVEINCTRPNNNTRKSIHIGPGRAFYTGTGEI 317
Qy 301 LGNIROAHCNISRAQWNTTQQIATTLREOPG-NKTIAFNOSGGDPEIVMHSFNCGGEF 359
Db 318 IGDIRQAHCHNISRTKWNLTNQIATLKEQGNKNTIVFQSSGGDPEIVMHSFNCGGEF 377
Qy 360 FYCNSTOLFNSAMVNTSGTWSVTRKQKDTG-DIITLPCRIKQIINRWQVVGKAMYALPI 418
Db 378 FYCNSTOLFNSAMVNTSGTWSVTRKQKDTG-DIITLPCRIKQIINRWQVVGKAMYALPI 435
Qy 419 KGLIRCSSNITGLLLTRDGGGENTTEIFRPGGDMRDNMRSELYKYKVKVIEPLGVA 478
Db 436 RGQIRCSSNITGLLLTRDGGGENTTEIFRPGGDMRDNMRSELYKYKVKVIEPLGVA 495
Qy 479 KAKRVVQREKRAVGMGLGAMFLGFLGAAGSTMATSMALTVQARQLLSGIVQOQNLLRA 538
Db 496 KAKRVVQREKRAVGMGLGAMFLGFLGAAGSTMATSMALTVQARQLLSGIVQOQNLLRA 555
Qy 539 IKAQOHLLOLTVMGIKOLQARILAVERYLKDQQLLGFWGCSSGKLICTTAVPWNASWSNKT 598
Db 556 IEAQOHLLOLTVMGIKOLQARILAVERYLKDQQLLGFWGCSSGKLICTTAVPWNASWSNKT 615
Qy 599 LDQIWNMTWMEWDREIDNTHLYTLIESONQOEKNOQELLDKWSL 649
Db 616 LDQIWNMTWMEWDREIDNTHLYTLIESONQOEKNOQELLDKWSL 666

RESULT 9
US-10-190-435-2
; Sequence 2, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 842
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SF162
US-10-190-435-2

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Query Match 83.0%; Score 2883.5; DB 4; Length 842;
Best Local Similarity 83.3%; Pred. No. 1.7e-219;
Matches 544; Conservative 40; Mismatches 38; Indels 31; Gaps 7;

Qy 3 LWTVYGVVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQVILENTENF 62
Db 28 LWTVYGVVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQVILENTENF 87
Qy 63 NMKNKNVQMHEDIISLWDSQSLKPCVKLTPLCVTLNCTDLNNTNTTNTTSLIIVVWQ 122
Db 88 NMKNKNVQMHEDIISLWDSQSLKPCVKLTPLCVTLNCTDLNNTNTKSSN-----WKE 141
Qy 123 RGKGMNRCFNITTSIRDKVQREYALFYKLDVEPIDDKNNTNTNTKYLINCNSTVIITQ 182
Db 142 MDRGEIKNCSFKVTTISIRNKQKEYALFYKLDVVPIDN-----DNTSYKLINCNSTVIITQ 196
Qy 183 ACPKVSFEPIPIHYCTPTGALLKCNDDKFGNGTGPCTNVSTVQCTHGIRPVVSTQLLNG 242
Db 197 ACPKVSFEPIPIHYCAPAGFAILKCNDDKFGNGTGPCTNVSTVQCTHGIRPVVSTQLLNG 256
Qy 243 SLAEVEVIRSNFTDNNKIIIVQLNVSVEINCTRPNNNTRKVTILGPGRVWVTTGELLG 302

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Db 257 SLAEVEVIRSENFTDNNKIIIVQLKESVEINCTRPNNNTRKSIITIGPGRAFYTATGDI 316
Qy 303 NIRAQHCNISRAQWNTTQQIATTLREOPG-NKTIAFNOSGGDPEIVMHSFNCGGEF 362
Db 317 DIRQAHCHNISRTKWNLTNQIATLKEQGNKNTIVFQSSGGDPEIVMHSFNCGGEF 376
Qy 363 NSTOLFNSAMVNTSGTWSVTRKQKDTG-DIITLPCRIKQIINRWQVVGKAMYALP 417
Db 377 NSTOLFNSAMVNTSGTWSVTRKQKDTG-DIITLPCRIKQIINRWQVVGKAMYALP 423
Qy 418 IKGLIRCSSNITGLLLTRDGGGENTTEIFRPGGDMRDNMRSELYKYKVKVIEPLGVA 476
Db 424 IRQIRCSSNITGLLLTRDGGGENTTEIFRPGGDMRDNMRSELYKYKVKVIEPLGVA 483
Qy 477 PTAKRVVQREKRAVGMGLGAMFLGFLGAAGSTMATSMALTVQARQLLSGIVQOQNLL 536
Db 484 PTAKRVVQREKRAVGMGLGAMFLGFLGAAGSTMATSMALTVQARQLLSGIVQOQNLL 542
Qy 537 RAIKAQOHLLOLTVMGIKOLQARILAVERYLKDQQLLGFWGCSSGKLICTTAVPWNASWSN 596
Db 543 RAIKAQOHLLOLTVMGIKOLQARILAVERYLKDQQLLGFWGCSSGKLICTTAVPWNASWSN 602
Qy 597 KTLDOQIWNMTWMEWDREIDNTHLYTLIESONQOEKNOQELLDKWSL 649
Db 603 KSLDQIWNMTWMEWDREIDNTHLYTLIESONQOEKNOQELLDKWSL 655

RESULT 10
US-10-241-009-2
; Sequence 2, Application US/10241009
; Publication No. US20030170614A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 2300-1621.21
; CURRENT APPLICATION NUMBER: US/10/241,009
; CURRENT FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 842
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SF162
US-10-241-009-2

```

```

Query Match 83.0%; Score 2883.5; DB 4; Length 842;
Best Local Similarity 83.3%; Pred. No. 1.7e-219;
Matches 544; Conservative 40; Mismatches 38; Indels 31; Gaps 7;

Qy 3 LWTVYGVVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQVILENTENF 62
Db 28 LWTVYGVVWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPQVILENTENF 87
Qy 63 NMKNKNVQMHEDIISLWDSQSLKPCVKLTPLCVTLNCTDLNNTNTTNTTSLIIVVWQ 122
Db 88 NMKNKNVQMHEDIISLWDSQSLKPCVKLTPLCVTLNCTDLNNTNTKSSN-----WKE 141
Qy 123 RGKGMNRCFNITTSIRDKVQREYALFYKLDVEPIDDKNNTNTNTKYLINCNSTVIITQ 182
Db 142 MDRGEIKNCSFKVTTISIRNKQKEYALFYKLDVVPIDN-----DNTSYKLINCNSTVIITQ 196
Qy 183 ACPKVSFEPIPIHYCTPTGALLKCNDDKFGNGTGPCTNVSTVQCTHGIRPVVSTQLLNG 242
Db 197 ACPKVSFEPIPIHYCAPAGFAILKCNDDKFGNGTGPCTNVSTVQCTHGIRPVVSTQLLNG 256
Qy 243 SLAEVEVIRSENFTDNNKIIIVQLNVSVEINCTRPNNNTRKVTILGPGRVWVTTGELLG 302

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Db 257 SLAEGVVRSENFTDNAKTIIVQLKESVEINCTRPNNTRKSIITIGPGRFYATGDIIG 316
Qy 303 NIROAHCHNISRAQWNTLQOIATTLRBOFGNKTIAPNOSGGDPPEIVMHSFNCGEFFYC 362
Db 317 DIROAHCHNISGEKWNNTLKQIVTKLQAOFGNKTIIVFKQSSGGDPPEIVMHSFNCGEFFYC 376
Qy 363 NSTOLFNSAWNT-----SNGTWSVTRKQKDTGDIITLPCRIKQIINRWQVGVKAWYALP 417
Db 377 NSTOLFNSAWNTIGPNNNGT-----ITLPCRIKQIINRWQVGVKAWYAPP 423
Qy 418 IKGLIRCSSNITGLLLTRDGGGE-NQTTEIFRPGGDMRDNRSELKYKYVVKIEPLGVA 476
Db 424 IRGQIRCSSNITGLLLTRDGGGEISNTTEIFRPGGDMRDNRSELKYKYVVKIEPLGVA 483
Qy 477 PTKAKRRVVOREKRAVGLGAMFLGFLGAAGSTWGATSMALTVOARQLLSGIVQOQNLL 536
Db 484 PTKAKRRVVOREKRAV-TLGAMFLGFLGAAGSTWGARSLLTITVOARQLLSGIVQOQNLL 542
Qy 537 RAIKAQOHLQLTWGIIKQIARILAVERYLKQOQLLGFWCGSGKLICTTAVPWNASWN 596
Db 543 RAIKAQOHLQLTWGIIKQIARILAVERYLKQOQLLGFWCGSGKLICTTAVPWNASWN 602
Qy 597 KTLDOIWNMTMEWDREIDNYTHLYTLIESQKQKQOELLQLDKWSL 649
Db 603 KSLDOIWNMTMEWDREIDNYTHLYTLIESQKQKQOELLQLDKWSL 655

RESULT 11

US-10-190-434B-2
; Sequence 2, Application US/10190434B
; Publication No. US20030194800A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan
; APPLICANT: LIAN, Ying
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B
; FILE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 2300-1621.20
; CURRENT APPLICATION NUMBER: US/10/190,434B
; CURRENT FILING DATE: 2002-07-05
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 842
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SP162
US-10-190-434B-2

Query Match 83.0%; Score 2883.5; DB 4; Length 842;
Best Local Similarity 83.3%; Pred. No. 1.7e-219;
Matches 544; Conservative 40; Mismatches 38; Indels 31; Gaps 7;
Qy 3 LWVTYYGVVPWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPDPQEVLENVTENF 62
Db 28 LWVTYYGVVPWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPDPQEVLENVTENF 87
Qy 63 NMWKNMVQOEHEDIISLDQSLKPCVKLTPLCVTLNCTDLNTNTNTTSLIIVVWEQ 122
Db 88 NMWKNMVQOEHEDIISLDQSLKPCVKLTPLCVTLNCTDLNTNTNTTSLIIVVWEQ 141
Qy 123 RGKEMRNCSEFNITTSIRDKVQREYALFYKLDVEPIDDNKNNTNTKYLINCNTSVITQ 182
Db 142 MDRGEIKNCSFKVTTISIRNKQKEALFYKLDVVPIDN-----DNTSYKLINCNTSVITQ 196
Qy 183 ACPKVSPEPIPIHYCTPTGPFALLKCNCKKNGTGCTNVSTVQCTHGRPVVSTQOLLNG 242
Db 197 ACPKVSPEPIPIHYCAPAGFAILKCNCKKNGSGPCTNVSTVQCTHGRPVVSTQOLLNG 256
Qy 243 SLAEEVVRSENFTNNAKTIIVQLNVSVEINCTRPNNTRKSVITLGPGRVWYTTGILG 302
Db 257 SLAEEVVRSENFTDNAKTIIVQLKESVEINCTRPNNTRKSIITIGPGRFYATGDIIG 316

Qy 303 NIROAHCHNISRAQWNTLQOIATTLRBOFGNKTIAPNOSGGDPPEIVMHSFNCGEFFYC 362
Db 317 DIROAHCHNISGEKWNNTLKQIVTKLQAOFGNKTIIVFKQSSGGDPPEIVMHSFNCGEFFYC 376
Qy 363 NSTOLFNSAWNT-----SNGTWSVTRKQKDTGDIITLPCRIKQIINRWQVGVKAWYALP 417
Db 377 NSTOLFNSAWNTIGPNNNGT-----ITLPCRIKQIINRWQVGVKAWYAPP 423
Qy 418 IKGLIRCSSNITGLLLTRDGGGE-NQTTEIFRPGGDMRDNRSELKYKYVVKIEPLGVA 476
Db 424 IRGQIRCSSNITGLLLTRDGGGEISNTTEIFRPGGDMRDNRSELKYKYVVKIEPLGVA 483
Qy 477 PTKAKRRVVOREKRAVGLGAMFLGFLGAAGSTWGATSMALTVOARQLLSGIVQOQNLL 536
Db 484 PTKAKRRVVOREKRAV-TLGAMFLGFLGAAGSTWGARSLLTITVOARQLLSGIVQOQNLL 542
Qy 537 RAIKAQOHLQLTWGIIKQIARILAVERYLKQOQLLGFWCGSGKLICTTAVPWNASWN 596
Db 543 RAIKAQOHLQLTWGIIKQIARILAVERYLKQOQLLGFWCGSGKLICTTAVPWNASWN 602
Qy 597 KTLDOIWNMTMEWDREIDNYTHLYTLIESQKQKQOELLQLDKWSL 649
Db 603 KSLDOIWNMTMEWDREIDNYTHLYTLIESQKQKQOELLQLDKWSL 655

RESULT 12

US-10-190-305A-2
; Sequence 2, Application US/10190305A
; Publication No. US20030198621A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan
; APPLICANT: LIAN, Ying
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B AND/OR
; FILE OF INVENTION: TYPE C POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 2302-18702 / 18702.002
; CURRENT APPLICATION NUMBER: US/10/190,305A
; CURRENT FILING DATE: 2002-07-05
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 842
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SP162
US-10-190-305A-2

Query Match 83.0%; Score 2883.5; DB 4; Length 842;
Best Local Similarity 83.3%; Pred. No. 1.7e-219;
Matches 544; Conservative 40; Mismatches 38; Indels 31; Gaps 7;
Qy 3 LWVTYYGVVPWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPDPQEVLENVTENF 62
Db 28 LWVTYYGVVPWKEATTLFCASDAKAYDTEAHNVWATHACVPTNPDPQEVLENVTENF 87
Qy 63 NMWKNMVQOEHEDIISLDQSLKPCVKLTPLCVTLNCTDLNTNTNTTSLIIVVWEQ 122
Db 88 NMWKNMVQOEHEDIISLDQSLKPCVKLTPLCVTLNCTDLNTNTNTKSN-----WKE 141
Qy 123 RGKEMRNCSEFNITTSIRDKVQREYALFYKLDVEPIDDNKNNTNTKYLINCNTSVITQ 182
Db 142 MDRGEIKNCSFKVTTISIRNKQKEALFYKLDVVPIDN-----DNTSYKLINCNTSVITQ 196
Qy 183 ACPKVSPEPIPIHYCTPTGPFALLKCNCKKNGTGCTNVSTVQCTHGRPVVSTQOLLNG 242
Db 197 ACPKVSPEPIPIHYCAPAGFAILKCNCKKNGSGPCTNVSTVQCTHGRPVVSTQOLLNG 256
Qy 243 SLAEEVVRSENFTNNAKTIIVQLNVSVEINCTRPNNTRKSVITLGPGRVWYTTGILG 302
Db 257 SLAEEVVRSENFTDNAKTIIVQLKESVEINCTRPNNTRKSIITIGPGRFYATGDIIG 316

Qy	363	NSTOLFNSAWNT-----SNGTWSVTRKQKOTGDIIITLPCRIKOIINRWGVGKMYALP	417
Db	382	NSTOLFNSWNTNTIGPNNTNGT-----ITLPCRIKOIINRWGVGKMYAPP	428
Qy	418	IKGLIRCSSNITGLLLTRDGGGE-NOTTTEIFRPGGDMRDNRSSELYKYKVKVIEPLGYA	476
Db	429	IRGQIRCSSNITGLLLTRDGGKEISNTTEIFRPGGDMRDNRSSELYKYKVKVIEPLGYA	488
Qy	477	PTKAKRRVVOREKRAVGMGLGAMFLGFLGAAGSTWGATSMALTVOAROLLSSGIVOOQNLL	536
Db	489	PTKAKRRVVOREKRAV-TIGAMFLGFLGAAGSTWGAESLTLTVOAROLLSSGIVOOQNLL	547
Qy	537	RAIKAQOHLLOLTVMGIKLOQARIILAVERYLKDOQLLGFWGCSGKLTCTTAVPWNASWN	596
Db	548	RAIEAQOHLLOLTVMGIKLOQARVLAVERYLKDOQLLGIWGCSGKLTCTTAVPWNASWN	607
Qy	597	KTLDDQIWNNTWMDREIDNYTHLIYTLIEESNQOEKQOELLDDKWASL	649
Db	608	KSLDQITWNNTWMEVERSIDNYTNLIYTLIEESNQOEKNEQELLELDKWASL	660

RESULT 15

US-09-966-931-28
; Sequence 28, Application US/09966931

GENERAL INFORMATION:
APPLICANT: Berman, Phillip W.
Nakamura, Gerald R.
TITLE OF INVENTION: HIV Envelope Polypeptides
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP
STREET: 3 Embarcadero Center
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111

```

? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FastSeq for Windows Version 2.0

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/966,931
; FILING DATE: 27-Sep-2001
; CLASSIFICATION: <Unknown>
;

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PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/492,739
 FILING DATE: 2000-01-27
 ATTORNEY/AGENT INFORMATION:
 NAME: Haliday, Emily
 REGISTRATION NUMBER: 38903
 REFERENCE/DOCKET NUMBER: 14918-704
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-393-2000
 TELEFAX: 415-393-2386
 TEXT: <Unknown>

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? INFORMATION FOR SEQ ID NO: 28:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 850 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? SEQUENCE DESCRIPTION: SEQ ID NO: 28:

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Query Match	82.1%;	Score 2852;	DB 3;	Length 850;
Best Local Similarity	83.0%;	Pred. No. 5.5e-217;		
Matches 537;	Conservative	42;	Mismatches 52;	Indels 16;
				Gaps 7;

QY 3 LWVTYYGVVPVWKEATTTLFCASDAKAYDTEAHNVWATHACVPTNPQEVVLENTVNF 62

Db	33	LWTVVYGVVPWEKATTTLLFCASDAKAYDTEVHNWATHACVPTDPNPQETGLENTNF	92
Qy	63	NMKQNNVVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNTNNTTNTTSLISVWWEQ	122
Db	93	NMKQNNVVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDL--KNAITNTTSS-----WGK	146
Qy	123	RGKEMENCSFNITTSIRDKVQREYALFYKLDVPEPIDDNKNTTNTKVRLLNCNITSVITO	182
Db	147	MERGEIKNCFSNVVTSIRDKMKNYALFYKLDVVVPIDN-----DNTSYRLISCNITSVITO	201
Qy	183	ACPVSPEPIPIHYCTPTGPAALKCNDKFNKGTPCTNVSTVQCTHGIRPVVSTQLLING	242
Db	202	ACPVSPEPIPIHYCAPAGFALLKCRDKFNKGTPCTNVSTVQCTHGIRPVVSTQLLING	261
Qy	243	SLAEEVVIIRSENPNTNAKTIIVOLNVSEINCTRPNNHTRKRVTLGPRVYVYTGEILG	302
Db	262	SLAEEVVIIRSANFSDNAKTIIVOLNSESVEINCTRPNNTRRSIHIGPGRAYATGEIIG	321
Qy	303	NIROAHCHNISRAQWNNTLQOIATLREOFGNKTTAFNOSGGDPEIVMHSFNCGGEPPYC	362
Db	322	DIROAHCHNLSTKWNNTLKQIVTKLREHF--NKTIVFNHSSGGDPEIVMHSFNCGGEPPYC	380
Qy	363	NSTQLFNSAMNVTNSGTWSTVRKOKDTGDIITPLCRIKQIINRWQVVGKAMYALPIKGLI	422
Db	381	NTTPLFNSWNYYI--TWNTEGSDTGRNITLQCRIKQIINRWQVVGKAMYALPIRQOI	438
Qy	423	RCSNITGLLLTRDGGENOTTEIFRPGGDMRDNRSELYKYKVXKIEPLGVAPTAKAR	482
Db	439	RCSNITGLLLTRD--GNNSETEIFRPGGDMRDNRSELYKYKVXKIEPLGVAPTAKAR	497
Qy	483	RVVQREKRAYMGLGAMFLGPLGAAGSTWGTATSMALTVOAROLLGSIVOOQNNLRAIKAO	542
Db	498	RVVQREKRAYG--IGAVFLGPLGAAGSTWGTAAVSVTLTVOARILLGSIVOOQNNLRAIEAE	556
Qy	543	QHLLQLTVWGIKQIQARILAVERYLKDQQLLGFWGCCKLICCTTAVPWNASWSNKTLDOI	602
Db	557	QHLLQLTVWGIKQIQARVLAVERYLKDQQLLGIWGCCKLICCTTAVPWNASWSNKSLDKI	616
Qy	603	WNNMTWMDREIDNTYHTLLYTLIEESQOQEKQOELLQDJKWASL	649
Db	617	WNNMTWMEWEREIDNTYSLTYSILIEESQOQEKNEQELLELDJKWASL	663

Search completed: March 7, 2006, 17:56:38
Job time : 212.547 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2006, 17:53:05 ; Search time 24.8879 Seconds
(without alignments)
521.549 Million cell updates/sec

Title: US-09-938-406-1_COPY_33_681

Perfect score: 3474

Sequence: 1 ANLWTVYGVVWKEATTT.....ONQEKNOQELLQDKWASL 649

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 135346 seqs, 20000420 residues

Total number of hits satisfying chosen parameters: 135346

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

1: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2809.5	80.9	856	6	US-10-510-947-8
2	2809.5	80.9	856	7	US-11-042-988-13
3	2809.5	80.9	856	7	US-11-135-235-1
4	2756.5	79.3	681	7	US-11-014-842A-25
5	2756.5	79.3	869	7	US-11-014-842A-27
6	2668.5	76.8	689	7	US-11-014-842A-29
7	2668.5	76.8	857	7	US-11-014-842A-31
8	2509.5	72.2	613	7	US-11-014-842A-33
9	2509.5	72.2	801	7	US-11-014-842A-35
10	2489	71.6	854	7	US-11-022-562-219
11	2421.5	69.7	601	7	US-11-014-842A-37
12	2421.5	69.7	789	7	US-11-014-842A-39
13	1140	32.8	879	7	US-11-022-562-340
14	1112.5	32.0	860	7	US-11-022-562-217
15	653	18.8	145	7	US-11-084-858-11
16	511.5	14.7	379	7	US-11-116-203-3
17	436.5	12.6	146	7	US-11-084-858-10
18	330.5	9.5	220	7	US-11-151-598-1
19	330.5	9.5	225	7	US-11-151-598-7
20	330.5	9.5	225	7	US-11-151-598-8
21	330.5	9.5	227	7	US-11-151-598-9
22	330.5	9.5	267	7	US-11-151-598-2
23	316	9.1	213	6	US-10-841-956A-19
24	275	7.9	151	7	US-11-022-562-215
25	265	7.6	102	6	US-10-841-956A-18

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Sequence 24, Appli
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Sequence 11, Appli
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Sequence 7, Appli
Sequence 37, Appli
Sequence 1, Appli
Sequence 4, Appli

26 189 5.4 40 7 US-11-151-598-3
27 184 5.3 44 7 US-11-187-687-24
28 183 5.3 41 7 US-11-107-364-34
29 172 5.0 36 7 US-11-151-598-11
30 171 4.9 37 6 US-10-841-956A-2
31 171 4.9 37 7 US-11-029-003-2
32 167 4.8 38 7 US-11-151-598-4
33 166 4.8 35 7 US-11-096-725-16
34 166 4.8 35 7 US-11-096-725-21
35 165 4.7 47 7 US-11-151-598-5
36 164 4.7 35 7 US-11-096-725-18
37 162 4.7 40 7 US-11-151-598-6
38 160 4.6 34 7 US-11-112-277-8
39 160 4.6 34 7 US-11-112-277-36
40 160 4.6 34 7 US-11-151-598-10
41 160 4.6 34 7 US-11-151-598-12
42 160 4.6 35 7 US-11-112-277-7
43 160 4.6 35 7 US-11-112-277-37
44 157 4.5 35 7 US-11-115-425-1
45 157 4.5 35 7 US-11-115-425-4

ALIGNMENTS

RESULT 1

US-10-510-947-8
; Sequence 8, Application US/10510947
; Publication No. US20050255123A1
; GENERAL INFORMATION:
; APPLICANT: The Trustees of the University of Pennsylvania
; APPLICANT: Wilson, James M.
; APPLICANT: Medina, Maria Fe C.
; APPLICANT: Kobinger, Gary
; TITLE OF INVENTION: Chimeric Ebola Virus Envelopes and Uses, Therefor
; FILE REFERENCE: UPN-02811PCT
; CURRENT APPLICATION NUMBER: US/10/510,947
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US 60/376,480
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/385,704
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/427,752
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 856
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-510-947-8

Query Match 80.9%; Score 2809.5; DB 6; Length 856;
Best Local Similarity 82.6%; Pred. No. 4.6e-251;
Matches 538; Conservative 38; Mismatches 56; Indels 19; Gaps 9;

Qy 3 LWTVYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 62
Db 34 LWTVYGVVWKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 93
Qy 63 NMWKNVQKHEDIISLWQSLKPCVKLPCLVTNLCTDLNTNTNTTSLSIIVVWQ 122
Db 94 NMWKNVQKHEDIISLWQSLKPCVKLPCLVSLKCTDL--KNDTNTSSSGRMIME- 150
Qy 123 RGKGEKNCFNITTSIRDKVQREYALFYKLDVSEPIDNKNNTNTKYLINCNVTITQ 182
Db 151 --KGEIKNCNFNITSIRGVQKEYAFYKLDIIPIDN-----DTSYKLTSCNVTITQ 203
Qy 183 ACPKVSPEPIPIHYCTPTGFAILLKNDKNGTGTCTNVSTVQCTHGIKRPVWSTOLLNG 242
Db 204 ACPKVSPEPIPIHYCAPAGFAILLKNNKTFNGTGTCTNVSTVQCTHGIKRPVWSTOLLNG 263
Qy 243 SLABEEVIRSENFNTNNAKTIIVQLNVSVSEINCTRPNNHTRKRVTL--GPGRVWYTTGEI 300

Db 264 SLAEEVIRSVNFTDNTAKTIIIVQLNTSVEINCTRPNNNTRKRIQRPGRFVTTIGKI 323
Qy 301 LGNIROAHCHNISRAQWNTLQOIATTLREQFG-NKTIAFNQSSGGDEPEIVMHSFNCGGEF 359
Db 324 -GNMROAHCHNISRAKWNNTLKQIASKUREQFGNKKTIIFKQSSGGDEPEIVTHSFNCGGEF 382
Qy 360 FYCNSOLFNSAWNVTSGTWSVTRKQKDTG-DIITLPCRKIQIINRWQVVGKAMYALPI 418
Db 383 FYCNSOLFNSW--FNSWTSGSNTGSDTITLPCRKIQIINRWQVVGKAMYAPPI 439
Qy 419 KGLIRCSNITGLLLTRDGGENOTTEIFRPGGDMRDNRSELYKYKVKIEPLGVAPT 478
Db 440 SGQIRCSNITGLLLTRDGGNSNESEIFRPGGDMRDNRSELYKYKVKIEPLGVAPT 499
Qy 479 KAKRRVQREKRAVGMFLGAGSTMGATSWALTVQARQLLSGIVQOQNLLRA 538
Db 500 KAKRRVQREKRAVG-IGALFLGAGSTMGASMTLTVQARQLLSGIVQOQNLLRA 558
Qy 539 IKAQHLLQLTVWGIKQIARILAVERYLKDQQLLGFWCGSGKLICTTAVPWNASWNSKT 598
Db 559 IEAQHLLQLTVWGIKQIARILAVERYLKDQQLLGFWCGSGKLICTTAVPWNASWNSKS 618
Qy 599 LDQIWNMTWMDREIDNYTHLYTLIESQOQEKNOQELLQDKWASL 649
Db 619 LEQIWNHTTWMDREINNYTSLIHSILIESQOQEKNEQELLELDKWASL 669

RESULT 2

US-11-042-988-13
; Sequence I3, Application US/11042988
; Publication No. US20050244818A1
; GENERAL INFORMATION:
; APPLICANT: SILICIANO, ROBERT
; APPLICANT: ZHANG, HAILI
; APPLICANT: ZHOU, YAN
; TITLE OF INVENTION: SINGLE CELL ANALYSIS OF HIV REPLICATION CAPACITY AND
; FILE REFERENCE: 62760(71699)
; CURRENT APPLICATION NUMBER: US/11/042,988
; CURRENT FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/540,716
; PRIOR FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 13
; LENGTH: 856
; TYPE: PRP
; ORGANISM: Human immunodeficiency virus type 1
US-11-042-988-13

Query Match 80.9%; Score 2809.5; DB 7; Length 856;
Best Local Similarity 82.6%; Pred. No. 4.6e-251;
Matches 538; Conservative 38; Mismatches 56; Indels 19; Gaps 9;
Qy 3 LWTVYGVVPWKKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 62
Db 34 LWTVYGVVPWKKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 93
Qy 63 NMWKNMVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTTNTTSLSIIVVWEQ 122
Db 94 NMWKNMVEQMHEDIISLWQSLKPCVKLTPLCVSLKCTDL--KNDTNTSSSGRIME- 150
Qy 123 RGKGMENCSFNITTSIRDKVQREYALFYKLDVEPDNDKNTNTNTKYRLINCNVTITQ 182
Db 151 --KGEIKNCSFNISTIRGKVQKEYAFYKLDIIPDN-----DTSYKLTSCNTSVITQ 203
Qy 183 ACPKVSFEPIPIHYCTPTGFPALLKCNKXGNGTGPCTNVSTVQCTHGIRPVWSTQLLNG 242
Db 204 ACPKVSFEPIPIHYCAPAGFAILKCNKTFNGTGPCTNVSTVQCTHGIRPVWSTQLLNG 263
Qy 243 ACPKVSFEPIPIHYCTPTGFPALLKCNKXGNGTGPCTNVSTVQCTHGIRPVWSTQLLNG 300
Db 264 SLAEEVIRSVNFTDNTAKTIIIVQLNTSVEINCTRPNNNTRKRIQRPGRFVTTIGKI 323
Qy 243 SLAEEVIRSVNFTDNTAKTIIIVQLNTSVEINCTRPNNNTRKRIQRPGRFVTTIGKI 300

Db 264 SLAEEVIRSVNFTDNTAKTIIIVQLNTSVEINCTRPNNNTRKRIQRPGRFVTTIGKI 323
Qy 301 LGNIROAHCHNISRAQWNTLQOIATTLREQFG-NKTIAFNQSSGGDEPEIVMHSFNCGGEF 359
Db 324 -GNMROAHCHNISRAKWNNTLKQIASKUREQFGNKKTIIFKQSSGGDEPEIVTHSFNCGGEF 382
Qy 360 FYCNSOLFNSAWNVTSGTWSVTRKQKDTG-DIITLPCRKIQIINRWQVVGKAMYALPI 418
Db 383 FYCNSOLFNSW--FNSWTSGSNTGSDTITLPCRKIQIINRWQVVGKAMYAPPI 439
Qy 419 KGLIRCSNITGLLLTRDGGENOTTEIFRPGGDMRDNRSELYKYKVKIEPLGVAPT 478
Db 440 SGQIRCSNITGLLLTRDGGNSNESEIFRPGGDMRDNRSELYKYKVKIEPLGVAPT 499
Qy 479 KAKRRVQREKRAVGMFLGAGSTMGATSWALTVQARQLLSGIVQOQNLLRA 538
Db 500 KAKRRVQREKRAVG-IGALFLGAGSTMGASMTLTVQARQLLSGIVQOQNLLRA 558
Qy 539 IKAQHLLQLTVWGIKQIARILAVERYLKDQQLLGFWCGSGKLICTTAVPWNASWNSKT 598
Db 559 IEAQHLLQLTVWGIKQIARILAVERYLKDQQLLGFWCGSGKLICTTAVPWNASWNSKS 618
Qy 599 LDQIWNMTWMDREIDNYTHLYTLIESQOQEKNOQELLQDKWASL 649
Db 619 LEQIWNHTTWMDREINNYTSLIHSILIESQOQEKNEQELLELDKWASL 669

RESULT 3

US-11-135-235-1
; Sequence 1, Application US/11135235
; Publication No. US20060019395A1
; GENERAL INFORMATION:
; APPLICANT: Marasco, Wayne
; TITLE OF INVENTION: Lenticral Vectors and Uses Thereof
; FILE REFERENCE: 20363-027
; CURRENT APPLICATION NUMBER: US/11/135,235
; CURRENT FILING DATE: 2005-05-23
; PRIOR APPLICATION NUMBER: 60/589,610
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 856
; TYPE: PRP
; ORGANISM: Human immunodeficiency virus type 1
US-11-135-235-1

Query Match 80.9%; Score 2809.5; DB 7; Length 856;
Best Local Similarity 82.6%; Pred. No. 4.6e-251;
Matches 538; Conservative 38; Mismatches 56; Indels 19; Gaps 9;
Qy 3 LWTVYGVVPWKKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 62
Db 34 LWTVYGVVPWKKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 93
Qy 63 NMWKNMVEQMHEDIISLWQSLKPCVKLTPLCVTLNCTDLNNTNTTNTTSLSIIVVWEQ 122
Db 94 NMWKNMVEQMHEDIISLWQSLKPCVKLTPLCVSLKCTDL--KNDTNTSSSGRIME- 150
Qy 123 RGKGMENCSFNITTSIRDKVQREYALFYKLDVEPDNDKNTNTNTKYRLINCNVTITQ 182
Db 151 --KGEIKNCSFNISTIRGKVQKEYAFYKLDIIPDN-----DTSYKLTSCNTSVITQ 203
Qy 183 ACPKVSFEPIPIHYCTPTGFPALLKCNKXGNGTGPCTNVSTVQCTHGIRPVWSTQLLNG 242
Db 204 ACPKVSFEPIPIHYCAPAGFAILKCNKTFNGTGPCTNVSTVQCTHGIRPVWSTQLLNG 263
Qy 243 SLAEEVIRSVNFTDNTAKTIIIVQLNTSVEINCTRPNNNTRKRIQRPGRFVTTIGKI 300
Db 264 SLAEEVIRSVNFTDNTAKTIIIVQLNTSVEINCTRPNNNTRKRIQRPGRFVTTIGKI 323
Qy 301 LGNIROAHCHNISRAQWNTLQOIATTLREQFG-NKTIAFNQSSGGDEPEIVMHSFNCGGEF 359

Db 324 -GNMQAHCHNISRAKWNNTLKQIASKLREQFGNNKTIIFKQSSGGDPPIVTHSFNCGGEF 382
 Qy 360 FYCNSTQLFNSAWNTSNGTVSRKQKDTG-DIITLPCRKQIINRWQVGVKAMALPI 418
 Db 383 FYCNSTQLFNSAWNTSNGTVSRKQKDTG-DIITLPCRKQIINRWQVGVKAMALPI 439
 Qy 419 KGLIRCSNITGLLTRDGGGNNOTTEIFRPGGDMRDNWRSELYKYKVVKEIPLGVAPT 478
 Db 440 SQIRCSNITGLLTRDGGGNNOTTEIFRPGGDMRDNWRSELYKYKVVKEIPLGVAPT 499
 Qy 479 KAKRVVQREKRAVGMGLGFLGAAAGSTMGATSMALTVOARQLLSGIVQOQNLLRA 538
 Db 500 KAKRVVQREKRAVGMGLGFLGAAAGSTMGATSMALTVOARQLLSGIVQOQNLLRA 558
 Qy 539 IKAQHLLQLTWGIKQIARILAVERYLKQOQLLGFPGCSGKLICTTAVPWNASWNTK 598
 Db 559 IEAQHLLQLTWGIKQIARILAVERYLKQOQLLGFPGCSGKLICTTAVPWNASWNTK 618
 Qy 599 LDOQWNNMTWMEWDREIDNYTHLYTLIESONQOEKNOQELLQDKWASL 649
 Db 619 LEQIWNHTTWMEWDREIDNYTHLYTLIESONQOEKNOQELLQDKWASL 669
 RESULT 4
 US-11-014-842A-25
 ; Sequence 25, Application US/11014842A
 ; Publication No. US20060013826A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TANGY, FREDERIC
 ; APPLICANT: LORIN, CLARISSE
 ; APPLICANT: MOLLET, LUCILE
 ; APPLICANT: DELEBECQUE, FREDERIC
 ; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF
 ; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
 ; TITLE OF INVENTION: VACCINE COMPOSITIONS
 ; FILE REFERENCE: 2356.0093
 ; CURRENT APPLICATION NUMBER: US/11/014,842A
 ; CURRENT FILING DATE: 2004-12-20
 ; PRIOR APPLICATION NUMBER: PCT/EP03/07146
 ; PRIOR FILING DATE: 2003-06-20
 ; PRIOR APPLICATION NUMBER: EP 02291550.8
 ; PRIOR FILING DATE: 2002-06-20
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: Patent In Ver. 3.3
 ; SEQ ID NO 25
 ; LENGTH: 681
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus type 1
 US-11-014-842A-25

Query Match 79.3%; Score 2756.5; DB 7; Length 681;
 Best Local Similarity 79.4%; Pred. No. 2.6e-246;
 Matches 517; Conservative 60; Mismatches 53; Indels 21; Gaps 8;
 Qy 3 LMTVYGVVWKEATTLFCASDAKAYDTBAHNVWATHACVPTNPQEVLENVTENF 62
 Db 34 LMTVYGVVWKEATTLFCASDAKAYDTBAHNVWATHACVPTNPQEVLENVTENF 93
 Qy 63 NMWKNVQWHEHDIISLWDSLPKCVKLTPLCVTLNCTDLN-TNNTNTTSLIIVWE 121
 Db 94 NMWKNVQWHEHDIISLWDSLPKCVKLTPLCVTLNCTDLN-TNNTNTTSLIIVWE 149
 Qy 122 QRGKGMNCSFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTKYLINCNVTSVIT 181
 Db 150 MMEGEIKNCSFYITTSIRNKVKKEYALFNRLDVPV---KN-TSNTKYLINCNVTSVIT 205
 Qy 182 QACPKVSEPIPIHYCTPTGTGALLKCNKDKFNGTGPCTNVSTVQCTGIRPVVSTQLLN 241
 Db 206 QACPKVSEPIPIHYCVPAAGFAILKCNKNTFNGSGPCTNVSTVQCTGIRPVVSTQLLN 265
 Qy 242 GSLAEEVIRSEFTNNAKIIIVQLNVSEINCTRNPNHTRKRVTLGPRVWTTGELL 301
 Db 266 GSLAEEVIRSEFTNNAKIIIVQLNVSEINCTRNPNHTRKRVTLGPRVWTTGELL 325

Qy 302 GNIRQAHCHNISRAKWNNTLKQIATTLREQFNKTIIFKQSSGGDPPIVTHSFNCGGEFF 361
 Db 326 GNIRQAHCHNISRAKWNNTLKQIATTLREQFNKTIIFKQSSGGDPPIVTHSFNCGGEFF 385
 Qy 362 CNSTQLFNSAWNT--SNGTWSVTRKQKDTGDIITLPCRKQIINRWQVGVKAMALPIK 419
 Db 386 CNSTQLFNSAWNT--SNGTWSVTRKQKDTGDIITLPCRKQIINRWQVGVKAMALPIK 437
 Qy 420 GLIRCSNITGLLTRDGGGNNOT-TEIFRPGGDMRDNWRSELYKYKVVKEIPLGVAPT 478
 Db 438 GLIRCSNITGLLTRDGGGNNOT-TEIFRPGGDMRDNWRSELYKYKVVKEIPLGVAPT 497
 Qy 479 KAKRVVQREKRAVGMGLGFLGAAAGSTMGATSMALTVOARQLLSGIVQOQNLLRA 538
 Db 498 KAKRVVQREKRAVGMGLGFLGAAAGSTMGATSMALTVOARQLLSGIVQOQNLLRA 556
 Qy 539 IKAQHLLQLTWGIKQIARILAVERYLKQOQLLGFPGCSGKLICTTAVPWNASWNTK 598
 Db 557 IEAQHLLQLTWGIKQIARILAVERYLKQOQLLGFPGCSGKLICTTAVPWNASWNTK 616
 Qy 599 LDOQWNNMTWMEWDREIDNYTHLYTLIESONQOEKNOQELLQDKWASL 649
 Db 617 VDDIWNHTTWMEWDREIDNYTHLYTLIESONQOEKNOQELLQDKWASL 667

RESULT 5
 US-11-014-842A-27
 ; Sequence 27, Application US/11014842A
 ; Publication No. US20060013826A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TANGY, FREDERIC
 ; APPLICANT: LORIN, CLARISSE
 ; APPLICANT: MOLLET, LUCILE
 ; APPLICANT: DELEBECQUE, FREDERIC
 ; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF
 ; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
 ; TITLE OF INVENTION: VACCINE COMPOSITIONS
 ; FILE REFERENCE: 2356.0093
 ; CURRENT APPLICATION NUMBER: US/11/014,842A
 ; CURRENT FILING DATE: 2004-12-20
 ; PRIOR APPLICATION NUMBER: PCT/EP03/07146
 ; PRIOR FILING DATE: 2003-06-20
 ; PRIOR APPLICATION NUMBER: EP 02291550.8
 ; PRIOR FILING DATE: 2002-06-20
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: Patent In Ver. 3.3
 ; SEQ ID NO 27
 ; LENGTH: 869
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus type 1
 US-11-014-842A-27

Query Match 79.3%; Score 2756.5; DB 7; Length 869;
 Best Local Similarity 79.4%; Pred. No. 3.7e-246;
 Matches 517; Conservative 60; Mismatches 53; Indels 21; Gaps 8;
 Qy 3 LMTVYGVVWKEATTLFCASDAKAYDTBAHNVWATHACVPTNPQEVLENVTENF 62
 Db 34 LMTVYGVVWKEATTLFCASDAKAYDTBAHNVWATHACVPTNPQEVLENVTENF 93
 Qy 63 NMWKNVQWHEHDIISLWDSLPKCVKLTPLCVTLNCTDLN-TNNTNTTSLIIVWE 121
 Db 94 NMWKNVQWHEHDIISLWDSLPKCVKLTPLCVTLNCTDLN-TNNTNTTSLIIVWE 149
 Qy 122 QRGKGMNCSFNITTSIRDKVQREYALFYKLDVEPIDDKNTNTKYLINCNVTSVIT 181
 Db 150 MMEGEIKNCSFYITTSIRNKVKKEYALFNRLDVPV---KN-TSNTKYLINCNVTSVIT 205
 Qy 182 QACPKVSEPIPIHYCTPTGTGALLKCNKDKFNGTGPCTNVSTVQCTGIRPVVSTQLLN 241
 Db 206 QACPKVSEPIPIHYCVPAAGFAILKCNKNTFNGSGPCTNVSTVQCTGIRPVVSTQLLN 265

Db 150 MMEGEIKNCSPYITTSIRNKVKKEYALFNRLDVVPV---KN-TSNTKYRLISNTSVIT 205
Qy 182 QACPKVSEPIPIHYCTPTGFPALLKCNCKFNGTGPCTNVSTVQCTHGRPWSTQLLLN 241
Db 206 QACPKVSEPIPIHYCVFAGFALLKCNCKFNGTGPCTNVSTVQCTHGRPWSTQLLLN 265
Qy 242 GSLAEVVIRSEFTNNAKTIIVQLNVSVINCTRPNNHTRKRVTLGPGRVWTTGELL 301
Db 266 GSLAEEDIVIRSEFTDNVKTIIIVQLNESVVINCTRPNNNAEL-----DKWASAA--- 316
Qy 302 GNIRAHNCISRAQNNNTLQIATTLRQFGNKTIAFNQSSGGDEIIVMHSFNCGGEPFY 361
Db 317 ---RQAHNCISRAKNNNTLQIIVIKLREKFRNKTIAFNQSSGGDEIIVMHSFNCGGEPFY 373
Qy 362 CNSTQLFNSANNVT--SNGTWSVTRKQKDTGDIITLPCRKIQIINRWQVGVKAMYPK 419
Db 374 CNTAQLFNSVNWAGTNGT-----EGNDIITLQCRKIQIINMWQVGVKAMYPIT 425
Qy 420 GLIRCSSNITGLLLTRDGGENOT--TEIFRPGGDMRDNRSELYKVKVIEPLGVAPT 478
Db 426 GQIRCSSNITGLLLTRDGGNSTETETETEIFRPGGDMRDNRSELYKVKVRIEPIGVAPT 485
Qy 479 KAKRVVQREKRAVGMGLGAMFLGFLGAAGSTMATSMALTVQARQLLSGIVQOQNNLLRA 538
Db 486 KAKRTVQREKRAVG-IGAVFLGFLGAAGSTMGAASVTLTVQARLLSGIVQOQNNLLRA 544
Qy 539 IKAQHLQLTVWGIKQIQAARILAVERYLKDQQLGFGWCSGKLICTTAVPWNASWSNKT 598
Db 545 IEAQNNMLRLTVWGIKQIQAARILAVERYLQDLQMGWCSGKLICTTSVPWNVSNKSV 604
Qy 599 LQIANNMTMWEDEIDNYTHLYITLIEESQNOQKQOELLQDLKWSL 649
Db 605 VDDIANNMTMWEDEIDNYTDYIYDLLEKSGTQOEKNEKELLELDKWSL 655

RESULT 8

US-11-014-842A-33

; Sequence 33, Application US/11014842A

; Publication No. US20060013826A1

; GENERAL INFORMATION:

; APPLICANT: TANGY, FREDERIC

; APPLICANT: LORIN, CLARISE

; APPLICANT: MOLLET, LUCILE

; APPLICANT: DELEBECQUE, FREDERIC

; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF

; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF

; TITLE OF INVENTION: VACCINE COMPOSITIONS

; FILE REFERENCE: 2356.0093

; CURRENT APPLICATION NUMBER: US/11/014.842A

; CURRENT FILING DATE: 2004-12-20

; PRIOR APPLICATION NUMBER: PCT/EP03/07146

; PRIOR FILING DATE: 2003-06-20

; PRIOR APPLICATION NUMBER: EP 02291550.8

; PRIOR FILING DATE: 2002-06-20

; NUMBER OF SEQ. ID NOS: 43

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 33

; LENGTH: 613

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

US-11-014-842A-33

Query Match 72.2%; Score 2509.5; DB 7; Length 613;
Best Local Similarity 72.6%; Pred. No. 1.5e-223;
Matches 472; Conservative 49; Mismatches 42; Indels 87; Gaps 5;

Qy 3 LWTVVYGVVWKEATTLTFCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTENF 62
Db 34 LWTVVYGVVWREATTLTFCASDAKAYDTEAHNVWATHACVPTDPNPQEVVLENVTENF 93
Qy 63 NWKNNMVEQMHEDIISLWDSQKPCVKLTPLCVTLNCTDLNTNTNTTSLSIIVVWEQ 122
Db 94 NWKNNMVDQMHEDIISLWDSLSKPCVKLTPLCVTL----- 129

Qy 123 RGKGMNCNCSFNITTSIRDKVQREYALFYKLDVEPIDDNKNNTNTNTKYRLINCNTSVITQ 182
Db 130 -----NCNTSVITQ 138
Qy 183 ACPKVSPEPIPIHYCTPTGFPALLKCNCKFNGTGPCTNVSTVQCTHGRPWSTQLLLN 242
Db 139 ACPKVSPEPIPIHYCVFAGFALLKCNCKFNGTGPCTNVSTVQCTHGRPWSTQLLLN 198
Qy 243 SLAEVVIRSEFTNNAKTIIVQLNVSVINCTRPNNHTRKRVTLGPGRVWTTGELL 302
Db 199 SLAEEDIVIRSEFTDNVKTIIIVQLNESVVINCTRPNNTRERLSIGPGRAFYARRNIIG 258
Qy 303 GNIRAHNCISRAQNNNTLQIATTLRQFGNKTIAFNQSSGGDEIIVMHSFNCGGEPFYC 362
Db 259 DIRAHNCISRAKNNNTLQIIVIKLREKFRNKTIAFNQSSGGDEIIVMHSFNCGGEPFYC 318
Qy 363 NSTOLFNSANNVT--SNGTWSVTRKQKDTGDIITLPCRKIQIINRWQVGVKAMYPK 420
Db 319 NTAQLFNSVNWAGTNGT-----EGNDIITLQCRKIQIINMWQVGVKAMYPITG 370
Qy 421 LIRCSSNITGLLLTRDGGENOT--TEIFRPGGDMRDNRSELYKVKVIEPLGVAPT 479
Db 371 QIRCSSNITGLLLTRDGGNSTETETETEIFRPGGDMRDNRSELYKVKVRIEPIGVAPT 430
Qy 480 KAKRVVQREKRAVGMGLGAMFLGFLGAAGSTMATSMALTVQARQLLSGIVQOQNNLLRAI 539
Db 431 KAKRTVQREKRAVG-IGAVFLGFLGAAGSTMGAASVTLTVQARLLSGIVQOQNNLLRAI 489
Qy 540 KAOHLQLTVWGIKQIQAARILAVERYLKDQQLGFGWCSGKLICTTAVPWNASWSNKT 599
Db 490 EAQNNMLRLTVWGIKQIQAARILAVERYLQDLQMGWCSGKLICTTSVPWNVSNKSV 549
Qy 600 LQIANNMTMWEDEIDNYTHLYITLIEESQNOQKQOELLQDLKWSL 649
Db 550 VDDIANNMTMWEDEIDNYTDYIYDLLEKSGTQOEKNEKELLELDKWSL 599

RESULT 9

US-11-014-842A-35

; Sequence 35, Application US/11014842A

; Publication No. US20060013826A1

; GENERAL INFORMATION:

; APPLICANT: TANGY, FREDERIC

; APPLICANT: LORIN, CLARISE

; APPLICANT: MOLLET, LUCILE

; APPLICANT: DELEBECQUE, FREDERIC

; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF

; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF

; TITLE OF INVENTION: VACCINE COMPOSITIONS

; FILE REFERENCE: 2356.0093

; CURRENT APPLICATION NUMBER: US/11/014.842A

; CURRENT FILING DATE: 2004-12-20

; PRIOR APPLICATION NUMBER: PCT/EP03/07146

; PRIOR FILING DATE: 2003-06-20

; PRIOR APPLICATION NUMBER: EP 02291550.8

; PRIOR FILING DATE: 2002-06-20

; NUMBER OF SEQ. ID NOS: 43

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 35

; LENGTH: 801

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

US-11-014-842A-35

Query Match 72.2%; Score 2509.5; DB 7; Length 801;
Best Local Similarity 72.6%; Pred. No. 2.1e-223;
Matches 472; Conservative 49; Mismatches 42; Indels 87; Gaps 5;

Qy 3 LWTVVYGVVWKEATTLTFCASDAKAYDTEAHNVWATHACVPTNPQEVVLENVTENF 62
Db 34 LWTVVYGVVWREATTLTFCASDAKAYDTEAHNVWATHACVPTDPNPQEVVLENVTENF 93

Qy 63 NWKNNMVEQMHEDIISLWDSKPCVKLTPLCVTLNCTDLNNTNTTNTTSLSIIVVWEQ 122
 Db 94 NWKNNMVDQMHEDIISLWDSKPCVKLTPLCVTLNCTDLNNTNTTNTTSLSIIVVWEQ 129
 Qy 123 RGKEMRNCSPNITTSIRDKVQREVALFYKLDVEPIIDNNKNTTNTKYRLINCNTSVITQ 182
 Db 130 -----NNTSVITQ 138
 Qy 183 ACQKVSFPIPIHYCTPTGFAALLKNDKFGTGTCTNVSTVQCTHGRPVVSTOLLNG 242
 Db 139 ACQKVSFQPIPIHYCVAGFAALLKNNKTNFNGSGPCTNVSTVQCTHGRPVVSTOLLNG 198
 Qy 243 SLABEEVIRSENFTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGILG 302
 Db 199 SLABEDIVIRSEDFTDNVKTIIVQLNVSEVINCTRPNNHTRKRVTLGPRVWYTTGILG 258
 Qy 303 NIROAHCHNISRAQWNTLQOIATTLREOFNGKTIAPNOSGGDEPEIVMHSFNCGGEFFYC 362
 Db 259 DIROAHCHNISRAQWNTLQOIVIKLREKFRNKTIAPNOSGGDEPEIVMHSFNCGGEFFYC 318
 Qy 363 NSTQLFNSAWNT--SNGTWSVTRKQKDTGDIITLPCRILQIINRWQVGVKAMVALPIK 420
 Db 319 NTAGLFNSTVNAVGTGT-----BGNDIITLQCRILQIINRWQVGVKAMVALPIK 370
 Qy 421 LIRCSSNITGLLLTRDGGENQT-TEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPTK 479
 Db 371 QIRCSSNITGLLLTRDGGENSTETETEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPTR 430
 Qy 480 AKRRVQREKRAVGMGLGAMFLGFGAAGSTMGATSMALTVOARQLLSGIVQOQNLLRAI 539
 Db 431 AKRRVQREKRAVG-IGAVFLGFGAAGSTMGASVLTVOARQLLSGIVQOQNLLRAI 489
 Qy 540 KAOQHLLQLTVMGILQOLQARILAVERYLKDQQLLGFWCGSGKLICTTAVPWNASWSNKT 599
 Db 490 EAQNMURLTVMGILQOLQARILAVERYLKDQQLLGFWCGSGKLICTTAVPWNASWSNKT 549
 Qy 600 DQIWNNTMWEDEIDNYTHLIYTLIEESQOQEKNOQELLQDKWASL 649
 Db 550 DQIWNNTMWEDEIDNYTHLIYTLIEESQOQEKNOQELLQDKWASL 599

RESULT 10

US-11-022-562-219
 ; Sequence 219, Application US/11022562
 ; Publication No. US20050249742A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruprecht, Ruth M.
 ; APPLICANT: Shisong, Jiang
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
 ; FILE REFERENCE: DFN-043CN
 ; CURRENT APPLICATION NUMBER: US/11/022,562
 ; CURRENT FILING DATE: 2004-12-22
 ; PRIOR FILING DATE: 2003-06-27
 ; PRIOR FILING DATE: 2003-06-27
 ; PRIOR FILING DATE: 2002-06-27
 ; NUMBER OF SEQ ID NOS: 340
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 219
 ; LENGTH: 854
 ; TYPE: PRT
 ; ORGANISM: Human Immunodeficiency Virus
 US-11-022-562-219

Query Match 71.6%; Score 2489; DB 7; Length 854;
 Best Local Similarity 70.4%; Pred. No. 1.8e-221;
 Matches 459; Conservative 73; Mismatches 100; Indels 20; Gaps 6;
 Qy 2 NLWTVYGVVPMKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTEN 61
 Db 32 NLWTVYGVVPMKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTEN 91

Qy 62 FNMKNNMVEQMHEDIISLWDSKPCVKLTPLCVTLNCTDLNNTNTTNTTSLSIIVVWE 121
 Db 92 FNMKNNMVDQMHEDIISLWDSKPCVKLTPLCVTLNCTDLNNTNTTNTTSLSIIVVWE 147
 Qy 122 ORKGEWRNCSPNITTSIRDKVQREVALFYKLDVEPIIDNNKNTTNTKYRLINCNTSVIT 181
 Db 148 NNTSDMKNSCFNATTEVTDKIRKENALFYTLDIVPLDENQ---NNSNYRLINCNTSKVT 204
 Qy 182 QACPVSFPIPIHYCTPTGFAALLKNDKFGTGTCTNVSTVQCTHGRPVVSTOLLNG 241
 Db 205 QACPVSFQPIPIHYCVAGFAALLKNNKTNFNGSGPCTNVSTVQCTHGRPVVSTOLLNG 264
 Qy 242 GSLEBEVIRSENFTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGILG 301
 Db 265 GSLEBEVIRSENFTNNAKTIIVQLNVSEINCTRPNNHTRKRVTLGPRVWYTTGILG 324
 Qy 302 GNTROAHCHNISRAQWNTLQOIATTLREOFNGKTIAPNOSGGDEPEIVMHSFNCGGEFFY 361
 Db 325 GDIROAHCHNISRAQWNTLQOIVIKLREKFRNKTIAPNOSGGDEPEIVMHSFNCGGEFFY 384
 Qy 362 NSTQLFNSAWNT--SNGTWSVTRKQKDTGDIITLPCRILQIINRWQVGVKAMVALPIK 419
 Db 385 NTSLSFNNTYRPTYPNGT-----ESNSTITLQCRILQIINRWQVGVKAMVALPIK 436
 Qy 420 GLIRCSSNITGLLLTRDGG-GENOTTEIFRPGGDMRDNRSELYKYKVKVIEPLGVAP 477
 Db 437 GKITCKSNITGLLLTRDGGNGGNTATEIFRPGGDMRDNRSELYKYKVKVIEPLGVAP 496
 Qy 478 TKARRVQREKRAVGMGLGAMFLGFGAAGSTMGATSMALTVOARQLLSGIVQOQNLLRAI 537
 Db 497 TGARRVQREKRAVG-IGAVFLGFGAAGSTMGASITLTVOARQLLSGIVQOQNLLRAI 555
 Qy 538 AKAQOHLQLTVMGILQOLQARILAVERYLKDQQLLGFWCGSGKLICTTAVPWNASWSNK 597
 Db 556 AKAQOHLQLTVMGILQOLQARILAVERYLKDQQLLGFWCGSGKLICTTAVPWNASWSNK 615
 Qy 598 TLDQIWNNTMWEDEIDNYTHLIYTLIEESQOQEKNOQELLQDKWASL 649
 Db 616 SQADIWNNTMWEDEIDNYTHLIYTLIEESQOQEKNOQELLQDKWASL 667

RESULT 11

US-11-014-842A-37
 ; Sequence 37, Application US/11014842A
 ; Publication No. US20060013826A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TANGY, FREDERIC
 ; APPLICANT: LORIN, CLARISSE
 ; APPLICANT: MOLLET, LUCILE
 ; APPLICANT: DELEBEQUE, FREDERIC
 ; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF
 ; FILE REFERENCE: 2356.0093
 ; CURRENT APPLICATION NUMBER: US/11/014,842A
 ; CURRENT FILING DATE: 2004-12-20
 ; PRIOR FILING DATE: 2003-06-20
 ; PRIOR FILING DATE: 2003-06-20
 ; PRIOR FILING DATE: 2002-06-20
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: PatentIn Ver. 3.3
 ; SEQ ID NO 37
 ; LENGTH: 601
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus type 1
 US-11-014-842A-37

Query Match 69.7%; Score 2421.5; DB 7; Length 601;
 Best Local Similarity 71.1%; Pred. No. 1.9e-215;
 Matches 462; Conservative 44; Mismatches 45; Indels 99; Gaps 7;
 Qy 3 LWTVYGVVPMKEATTTLCASDAKAYDTEAHNVWATHACVPTNPQEVLENVTENF 62

Db 34 LWVYVYGVVWREATTTLFCASDAKAYDTEVHNWATHACVPTDPNPOEVVLGNVTENF 93
Qy 63 NMWKNMVQOMHEDIISLWDSKPCVKLTPLCVTLNCTDLNNTNTTNTTSLIIVVWEQ 122
Db 94 NMWKNMVQOMHEDIISLWDSKPCVKLTPLCVTL----- 129
Qy 123 RGKGBMRNCNFIITTSIRDKVOREVALFYKLDVEPIDDNKNTNTNTKYRLINCNTSVITQ 182
Db 130 -----NCNTSVITQ 138
Qy 183 ACPKVSFPIPIHYCTPTGPFALLKNDKFKNGTGTCTNVSTVQCTHGRPVVSTOLLNG 242
Db 139 ACPKVSFPIPIHYCVPAIFAILKCNKNTFNGSGPCTNVSTVQCTHGRPVVSTOLLNG 198
Qy 243 SLAEVWIRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPRVWYTTGELG 302
Db 199 SLAEEDIVIRSEDFDNDVKTIIIVQLNESVWVINCTRPNNAAEL-----DKWASAA 248
Qy 303 NIROAHNCISRAQWNTLQOIATTLREOFGNKTIAFNOSGGDPPEIVMHSFNCGGEFFYC 362
Db 249 --ROAHNCISRAQWNTLQOIVIKLREKFRNKTIAFNOSGGDPPEIVMHSFNCGGEFFYC 306
Qy 363 NSTOLFNSAMNVT--SNGTWSVTRKQKDTGDIITLPCRIKQIINRWQVVGKAMVALPIKG 420
Db 307 NTAQLFNSWNVAGTNGT-----EGNDIITLCRIKQIINRWQVVGKAMVALPIKG 358
Qy 421 LIRCSSNITGLLITRDGGGENOT--TEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPT 479
Db 359 QIRCSSNITGLLITRDGGNSTETETETEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPT 418
Qy 480 AKRRVOREKRAVGMGLAMFLGAGSTMGATSMALTVOAROLLGIVQOQNLLRAI 539
Db 540 KAOQHLLQTLVWGIKQARVLAVERYLKDOQLGFWGCSGKLTCTTAVPNNASWNSKTL 599
Qy 478 EAQNNMLTLVWGIKQARVLAVERYLKDOQLGFWGCSGKLTCTTAVPNNASWNSKSV 537
Db 538 DDWNNMTWMEWEREIDNIDYDYLLEKSTQOQEKKEKLELDKWSL 587

RESULT 12
US-11-014-842A-39
; Sequence 39, Application US/11014842A
; Publication No. US20060013826A1
; GENERAL INFORMATION:
; APPLICANT: TANGY, FREDERIC
; APPLICANT: LORIN, CLARISSE
; APPLICANT: MOLLET, LUCILE
; APPLICANT: DELEBEQUE, FREDERIC
; TITLE OF INVENTION: RECOMBINANT MEASLES VIRUSES EXPRESSING EPITOPES OF
; TITLE OF INVENTION: ANTIGENS OF RNA VIRUSES - USE FOR THE PREPARATION OF
; TITLE OF INVENTION: VACCINE COMPOSITIONS
; FILE REFERENCE: 2356.0093
; CURRENT APPLICATION NUMBER: US/11/014, 842A
; CURRENT FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: PCT/EP03/07146
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: EP 02291550.8
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 39
; LENGTH: 789
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-014-842A-39

Query Match 69.7%; Score 2421.5; DB 7; Length 789;
Best Local Similarity 71.1%; Pred. No. 2.8e-215;

Matches 462; Conservative 44; Mismatches 45; Indels 99; Gaps 7;
Qy 3 LWVYVYGVVWREATTTLFCASDAKAYDTEVHNWATHACVPTDPNPOEVVLGNVTENF 62
Db 34 LWVYVYGVVWREATTTLFCASDAKAYDTEVHNWATHACVPTDPNPOEVVLGNVTENF 93
Qy 63 NMWKNMVQOMHEDIISLWDSKPCVKLTPLCVTLNCTDLNNTNTTNTTSLIIVVWEQ 122
Db 94 NMWKNMVQOMHEDIISLWDSKPCVKLTPLCVTL----- 129
Qy 123 RGKGBMRNCNFIITTSIRDKVOREVALFYKLDVEPIDDNKNTNTNTKYRLINCNTSVITQ 182
Db 130 -----NCNTSVITQ 138
Qy 183 ACPKVSFPIPIHYCTPTGPFALLKNDKFKNGTGTCTNVSTVQCTHGRPVVSTOLLNG 242
Db 139 ACPKVSFPIPIHYCVPAIFAILKCNKNTFNGSGPCTNVSTVQCTHGRPVVSTOLLNG 198
Qy 243 SLAEVWIRSENFTNNAKTIIVQLNVSVEINCTRPNNHTRKRVTLGPRVWYTTGELG 302
Db 199 SLAEEDIVIRSEDFDNDVKTIIIVQLNESVWVINCTRPNNAAEL-----DKWASAA 248
Qy 303 NIROAHNCISRAQWNTLQOIATTLREOFGNKTIAFNOSGGDPPEIVMHSFNCGGEFFYC 362
Db 249 --ROAHNCISRAQWNTLQOIVIKLREKFRNKTIAFNOSGGDPPEIVMHSFNCGGEFFYC 306
Qy 363 NSTOLFNSAMNVT--SNGTWSVTRKQKDTGDIITLPCRIKQIINRWQVVGKAMVALPIKG 420
Db 307 NTAQLFNSWNVAGTNGT-----EGNDIITLCRIKQIINRWQVVGKAMVALPIKG 358
Qy 421 LIRCSSNITGLLITRDGGGENOT--TEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPT 479
Db 359 QIRCSSNITGLLITRDGGNSTETETETEIFRPGGDMRDNRSELYKYKVKVIEPLGVAPT 418
Qy 480 AKRRVOREKRAVGMGLAMFLGAGSTMGATSMALTVOAROLLGIVQOQNLLRAI 539
Db 540 KAOQHLLQTLVWGIKQARVLAVERYLKDOQLGFWGCSGKLTCTTAVPNNASWNSKTL 599
Qy 478 EAQNNMLTLVWGIKQARVLAVERYLKDOQLGFWGCSGKLTCTTAVPNNASWNSKSV 537
Db 538 DDWNNMTWMEWEREIDNIDYDYLLEKSTQOQEKKEKLELDKWSL 587

RESULT 13
US-11-022-562-340
; Sequence 340, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DFN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 340
; LENGTH: 879
; TYPE: PRT
; ORGANISM: Simian Immunodeficiency Virus
US-11-022-562-340

Query Match 32.8%; Score 1140; DB 7; Length 879;
Best Local Similarity 38.8%; Pred. No. 7.2e-97;

ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/084,858
FILING DATE: 21-Mar-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/000,321
FILING DATE: 04-Dec-2001
APPLICATION NUMBER: 09/131,551
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 58315/106/BEAK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-11-084-858-11

Query Match 18.8%; Score 653; DB 7; Length 145;
Best Local Similarity 87.5%; Pred. No. 5.2e-53;
Matches 119; Conservative 13; Mismatches 4; Indels 0; Gaps 0;
Qy 514 SMALTQARQLSGIVQOQNNLLRAIKAOQHLLQLTWGKIQARILAVERYLKDQOLL 573
Db 2 SLTLTVQARQLSGIVQOQNNLLRAIEAQHLLQLTWGKIQARVLAVERYLRDQOLL 61
Qy 574 GFWCGSGKLICTTAVPWNASNSKTLDOIWNMTTWMDREIDNYTHLYTLIESQNOQ 633
Db 62 GIWCGSGKLICTTAVPWNASNSKSLDIWDMTWQWREIDNTNTIYTLLESQNOQ 121
Qy 634 EKNOQELLQLDKWSL 649
Db 122 EKNEQELLELDKWSL 137

Search completed: March 7, 2006, 17:57:10
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